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(54) Title: NUCLEIC ACIDS, PROTEINS, AND ANTIBODIES

(57) Abstract: The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

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Nucleic Acids, Proteins, and Antibodies

[1] This application refers to a "Sequence Listing" that is provided only on electronic media in computer readable form pursuant to Administrative Instructions Section 801(a)(i). The Sequence Listing forms a part of this description pursuant to Rule 5.2 and Administrative Instructions Sections 801 to 806, and is hereby incorporated in its entirety.

[2] The Sequence Listing is provided as an electronic file (PTZ13PCT_seqList.txt, 5,421,455 bytes in size, created on January 13, 2001) on four identical compact discs (CD-R), labeled "COPY 1," "COPY 2," "COPY 3," and "CRF." The Sequence Listing complies with Annex C of the Administrative Instructions, and may be viewed, for example, on an IBM-PC machine running the MS-Windows operating system by using the V viewer software, version 2000 (see World Wide Web URL: <http://www.fileviewer.com>).

Field of the Invention

[3] The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to

these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Background of the Invention

[4] Enzymes comprise a large subset of proteins which function as catalysts for biochemical reactions. In fact, virtually every biochemical reaction involves the catalytic activity of an enzyme or enzymes. Most enzymes are located intracellularly, but there are a number of enzyme families which are either secreted into the extracellular space, or associated with the plasma membrane. Some enzymes, including the secreted digestive enzymes trypsin and pepsin, are produced as inactive precursors called zymogens, which require chemical modification to become active. In many cases, the catalytic activity of an enzyme depends on its association with a cofactor. Cofactors may be organic molecules, termed coenzymes, or metal ions. Many coenzymes are derived from vitamins.

[5] Enzymes contain two important functional units: the substrate binding site, and the catalytic site. The substrate-binding site consists of a cleft which is geometrically complementary to the shape of the preferred substrate. In addition, the amino acid residues which form the substrate binding site have noncovalent interactions with the amino acids of the complementary substrate region. The catalytic site is the portion of the molecule that facilitates the biochemical reaction once the substrate is bound to the enzyme. For a more extensive discussion of enzyme properties, see Biochemistry, Voet and Voet (1990); and Molecular Cell Biology, 2nd Edition, Darnell et al. (1990).

[6] The International Union of Biochemistry and Molecular Biology (IUBMB) has established enzyme nomenclature guidelines to provide an organizational framework to the growing field of enzymology (see Enzyme Nomenclature, Academic Press (1992), or the IUBMB Nomenclature Committee web site at the URL address: <http://www.chem.qmw.ac.uk/iubmb/enzyme>). According to the IUBMB guidelines, all enzymes can be categorized by the chemical reaction they catalyze. Documented enzymes are assigned an identifier which takes the form of "EC [A.B.C.D]", where A is one of the major functional classes of enzymes (1 through 6; see below); B and C designate increasingly specific

subgroups of enzymatic reactions; and D represents the arbitrary number of an individual member of a given category. As an example, the enzyme acetylcholinesterase is designated EC 3.1.1.7, because it is a member of the class of hydrolases (EC 3.-.-.-), acting on ester bonds (EC 3.1.-.-), in the subgroup of carboxylic ester hydrolases (EC 3.1.1.-), and it is assigned number 7. Descriptions of the six major functional classes, including notable examples of each, follow below.

Oxidoreductases (EC 1.-.-.-)

[7] Enzymes of this class catalyze oxidation-reduction reactions. Sub-classification is according to the substrate group oxidized (e.g., CH-OH, CH-CH, and CH-NH₂, to name but a few). A representative member of this enzyme class is long-chain-alcohol dehydrogenase (EC 1.1.1.192), which is involved in lipid metabolism. Deficient activity of this enzyme has been shown to be the primary cause of Sjogren-Larsson syndrome, an autosomal recessive disorder characterized by the presence of ichthyosis, mental retardation, and spasticity (Rizzo *et al.*, *J. Clin. Invest.* 81: 738-744 (1988)).

Transferases (EC 2.-.-.-)

[8] Catalytic reactions of transferases are characterized by the transfer of a chemical group from a "donor" molecule to an "acceptor" molecule. Transferases can be subgrouped according to the chemical group transferred. For example, amino transferases (EC 2.6.-.-) transfer nitrogenous groups, and methyltransferases (EC 2.1.1.-) transfer methyl groups. Often the transferred group is donated by a coenzyme. A major subgroup of transferase enzymes are the protein kinases (EC 2.7.-.-), which catalyze the transfer of a phosphate group from ATP to a substrate protein. Protein kinases, such as calcium/calmodulin dependent (CaM) kinase II (EC 2.7.1.123), are known to play important roles in signal transduction pathways (Kennedy, *Brain Res Brain Res Rev* 26(2-3):243-57 (1998)). Other transferases are involved in metabolic processes. For example, guanidinoacetate N-methyltransferase (GAMT; EC 2.1.1.2), converts guanidinoacetate into creatine, which is essential for the maintenance of energy reserves in the form of ATP. GAMT deficiency causes neurological impairments which may include progressive extrapyramidal movement disorders, seizures, developmental delay, and muscular dystonia (Stockler *et al.*, *Pediat. Res.* 36:409-413 (1994)).

Hydrolases (EC 3.-.-.)

[9] Enzymes of this class catalyze the splitting of a substrate into two fragments by the addition of a water molecule; the water's hydroxyl group being incorporated in one fragment and the hydrogen atom in the other. Hydrolases can be subcategorized according to the chemical bond involved. For example, peptidases (EC 3.4.-.-; also known as proteases) are hydrolases which catalyze the breaking of peptide bonds. Pepsin (EC 3.4.23.1), a digestive protease which has been implicated in a number of gastrointestinal disorders, is an example of a proteolytic hydrolase enzyme (see, for example, Hirschowitz, *Yale J. Biol. Med.* 72(2-3):133-43 (1999), and Del Bianco et al., *Dig. Liver Dis.* 32(1):12-9 (2000)). Deficient activity of beta-glucocerebrosidase (EC 3.2.1.45), an O-glycosyl hydrolase, is associated with Gaucher's disease. Symptoms of Gaucher's disease include bone lesions, skin pigmentation, enlargement of the liver and spleen, and, in some cases, neurological impairments.

Lyases (EC 4.-.-.)

[10] Lyases cleave C-C, C-O, C-N, and other bonds by means other than hydrolysis or oxidation. The reverse reaction is performed by a synthetase. Histidine decarboxylase (EC 4.1.1.22) is a carboxy-lyase that converts histidine to histamine, a biogenic amine involved in a number of physiologic processes, including inflammation, allergic responses, neurotransmission, and gastric acid secretion. The phosphorus-oxygen lyase, adenylate cyclase (EC 4.6.1.1), is an intracellular enzyme which acts on ATP to form adenosine 3', 5'-cyclic phosphate (cAMP), a second messenger activator of protein kinase activity.

Isomerases (EC 5.-.-.)

[11] Members of this class of enzymes catalyze geometric or structural changes within a molecule to form an isomer. Subclasses of isomerases include racemases / epimerases (EC 5.1.-.-), *cis-trans*- isomerases (EC 5.2.-.-), intramolecular isomerases (EC 5.3.-.-), intramolecular transferases (EC 5.4.-.-), and intramolecular lyases (EC 5.5.-.-). Protein disulfide isomerase (PDI; EC 5.3.4.1) catalyzes the intramolecular rearrangement of disulfide bonds, thus contributing to the folding of newly-synthesized proteins at the endoplasmic reticulum (see, for example, Luz and Lennarz, *EXS* 77:97-117 (1996)). Autoantibodies to PDI have been implicated in hepatic disorders (Nagayama et al., *J Toxicol Sci* Aug;19(3):163-9 (1994)).

Ligases (EC 6.-.-.-)

[12] Ligase enzymes catalyze the formation of a bond between two substrate molecules, coupled with the hydrolysis of a pyrophosphate bond in ATP or a similar triphosphate. A well characterized example of this class is DNA ligase 1 (EC 6.5.1.1), which catalyzes the joining of DNA fragments (via the formation of a phosphodiester bond) during DNA replication, recombination, and repair. Mutations in the gene encoding DNA ligase 1 have been linked to immunodeficiency disorders and hypersensitivity to DNA-damaging agents (Barnes et al., *Cell*, 69, 495-503 (1992)).

[13] The discovery of new human enzyme polynucleotides, the polypeptides encoded by them, and antibodies that immunospecifically bind these polypeptides, satisfies a need in the art by providing new compositions which are useful in the diagnosis, treatment, prevention and/or prognosis of a range of conditions, including but not limited to cancer, immunodeficiencies, neurological disorders, and metabolic disorders.

Summary of the Invention

[14] The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Detailed Description

Tables

[15] Table 1A summarizes some of the polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) and contig nucleotide sequence identifier (SEQ ID NO:X)) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby. The first column provides the gene number in the application for each clone identifier. The second column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence disclosed in Table 1A. The third column provides a unique contig identifier, "Contig ID:" for each of the contig sequences disclosed in Table 1A. The fourth column provides the sequence identifier, "SEQ ID NO:X", for each of the contig sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:X that delineate the preferred open reading frame (ORF) that encodes the amino acid sequence shown in the sequence listing and referenced in Table 1A as SEQ ID NO:Y (column 6). Column 7 lists residues comprising predicted epitopes contained in the polypeptides encoded by each of the preferred ORFs (SEQ ID NO:Y). Identification of potential immunogenic regions was performed according to the method of Jameson and Wolf (CABIOS, 4; 181-186 (1988)); specifically, the Genetics Computer Group (GCG) implementation of this algorithm, embodied in the program PEPTIDESTRUCTURE (Wisconsin Package v10.0, Genetics Computer Group (GCG), Madison, Wisc.). This method returns a measure of the probability that a given residue is found on the surface of the protein. Regions where the antigenic index score is greater than 0.9 over at least 6 amino acids are indicated in Table 1A as "Predicted Epitopes". In particular embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the predicted epitopes described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. Column 8, "Tissue Distribution" shows the expression profile of tissue, cells, and/or cell line libraries which express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the key provided in

Table 4. Expression of these polynucleotides was not observed in the other tissues and/or cell libraries tested. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon), represents the number of times a sequence corresponding to the reference polynucleotide sequence (e.g., SEQ ID NO:X) was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression. Column 9 provides the chromosomal location of polynucleotides corresponding to SEQ ID NO:X. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Given a presumptive chromosomal location, disease locus association was determined by comparison with the Morbid Map, derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM™. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). If the putative chromosomal location of the Query overlaps with the chromosomal location of a Morbid Map entry, an OMIM identification

number is disclosed in column 10 labeled "OMIM Disease Reference(s)". A key to the OMIM reference identification numbers is provided in Table 5.

[16] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

[17] Table 2 summarizes homology and features of some of the polypeptides of the invention. The first column provides a unique clone identifier, "Clone ID NO:Z", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" corresponding to contigs in Table 1A and allowing for correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:X", for the contig polynucleotide sequence. The fourth column provides the analysis method by which the homology/identity disclosed in the Table was determined. Comparisons were made between polypeptides encoded by the polynucleotides of the invention and either a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM") as further described below. The fifth column provides a description of the PFAM/NR hit having a significant match to a polypeptide of the invention. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, "Score/Percent Identity", provides a quality score or the percent identity, of the hit disclosed in columns five and six. Columns 8 and 9, "NT From" and "NT To" respectively, delineate the polynucleotides in "SEQ ID NO:X"

that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth and sixth columns. In specific embodiments polypeptides of the invention comprise, or alternatively consist of, an amino acid sequence encoded by a polynucleotide in SEQ ID NO:X as delineated in columns 8 and 9, or fragments or variants thereof.

[18] The PFAM identification disclosed in Table 2, columns 5 and 6, communicates both the function and enzymatic activity of polypeptides corresponding to the PFAM. Extensive documentation on PFAM families and individual members of these families are maintained in publicly accessible databases (see, for example the Sanger Centre PFAM web server at <http://www.sanger.ac.uk/> for a searchable PFAM database). Using this information, and included links to PROSITE, SWISSPROT, GenBank, and other sequence databases, one can routinely assign an EC (Enzyme Commission) code to the polypeptides. The EC code consists of 4 integers separated by decimal points that are used to classify enzymes, and indicate important information about cellular function and enzyme mechanism. The first digit indicates a broad group of enzyme mechanism (i.e. 1=oxidoreductases, 2=transferases). The second digit indicates the type of substrate the enzyme acts upon or a broad subcategory of the enzyme type (i.e. EC 1.6 oxidoreductases acting on NADH or NADPH, or 5.1=racemases and epimerases, a subtype of EC 5=isomerases). The third digit is used to distinguish further characteristics (EC 1.1.1 oxidoreductases acting on the CH-OH group of donors with NAD or NADP as the acceptor, versus EC 1.1.2 where a cytochrome acts as the acceptor) or is simply assigned as 1 for the all entries where further clarification is unnecessary (all members of EC 4.1, carbon-carbon lyases are in group 4.1.1). The final number designates a specific enzyme, for instance, EC 4.1.1.1 pyruvate decarboxylase, or EC 1.1.1.1 alcohol dehydrogenase. Thus, if all of the source sequences for the PFAM have EC codes of the form 1.1.3.X, where X is a positive integer, the polypeptide being evaluated is likely to have a similar EC code, and, in this example, will likely be an oxidoreductase acting on the CH-OH group of donors with oxygen as an acceptor.

[19] Furthermore, knowledge of PFAM identification and/or EC code for a polypeptide communicates enzymatic activity of the protein. This activity can routinely be confirmed using or modifying assays known in the art. Additionally, these assays may routinely be applied or modified to evaluate the enzymatic activity of fragments and variants of the invention. Further, these assays may routinely be applied or modified to

evaluate the ability of agonists or antagonists of the invention (e.g., agonistic or antagonistic antibodies) to enhance or reduce this enzymatic activity, respectively.

[20] Table 3 provides polynucleotide sequences that may be disclaimed according to certain embodiments of the invention. The first column provides a unique clone identifier, "Clone ID", for a cDNA clone related to contig sequences disclosed in Table 1A. The second column provides the sequence identifier, "SEQ ID NO:X", for contig sequences disclosed in Table 1A. The third column provides the unique contig identifier, "Contig ID:", for contigs disclosed in Table 1A. The fourth column provides a unique integer 'a' where 'a' is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, and the fifth column provides a unique integer 'b' where 'b' is any integer between 15 and the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. For each of the polynucleotides shown as SEQ ID NO:X, the uniquely defined integers can be substituted into the general formula of a-b, and used to describe polynucleotides which may be preferably excluded from the invention. In certain embodiments, preferably excluded from the invention are at least one, two, three, four, five, ten, or more of the polynucleotide sequence(s) having the accession number(s) disclosed in the sixth column of this Table (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone).

[21] Table 4 provides a key to the tissue/cell source identifier code disclosed in Table 1A, column 8. Column 1 provides the tissue/cell source identifier code disclosed in Table 1A, Column 8. Columns 2-5 provide a description of the tissue or cell source. Codes corresponding to diseased tissues are indicated in column 6 with the word "disease". The use of the word "disease" in column 6 is non-limiting. The tissue or cell source may be specific (e.g. a neoplasm), or may be disease-associated (e.g., a tissue sample from a normal portion of a diseased organ). Furthermore, tissues and/or cells lacking the "disease" designation may still be derived from sources directly or indirectly involved in a disease state or disorder, and therefore may have a further utility in that disease state or disorder. In numerous cases where the tissue/cell source is a library, column 7 identifies the vector used

to generate the library.

[22] Table 5 provides a key to the OMIM reference identification numbers disclosed in Table 1A, column 10. OMIM reference identification numbers (Column 1) were derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM, McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine, (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). Column 2 provides diseases associated with the cytologic band disclosed in Table 1A, column 9, as determined using the Morbid Map database.

[23] Table 6 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

[24] Table 7 shows the cDNA libraries sequenced, and ATCC designation numbers and vector information relating to these cDNA libraries.

[25] Table 8 provides a physical characterization of clones encompassed by the invention. The first column provides the unique clone identifier, "Clone ID NO:Z", for certain cDNA clones of the invention, as described in Table 1A. The second column provides the size of the cDNA insert contained in the corresponding cDNA clone.

Definitions

[26] The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

[27] In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

[28] As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence encoding SEQ ID NO:Y or a fragment or variant thereof; a nucleic acid sequence contained in SEQ ID NO:X (as described in column 3 of Table 1A) or the complement thereof; a cDNA sequence contained in Clone ID NO:Z (as described in column 2 of Table 1A and contained within a library deposited with the ATCC); a nucleotide sequence encoding the polypeptide encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or a fragment or variant thereof; or a nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complement thereof. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

[29] In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown, for example, in column 2 of Table 1A, each clone is identified by a cDNA Clone ID (identifier generally referred to herein as Clone ID NO:Z). Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. Furthermore, certain clones disclosed in this application have been deposited with the ATCC on October 5, 2000, having the ATCC designation numbers PTA 2574 and PTA 2575; and on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 7 provides a list of the deposited cDNA libraries. One can use the Clone ID NO:Z to determine the library source by reference to Tables 6 and 7. Table 7 lists the deposited cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone (Clone ID) isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1A correlates the Clone ID names with SEQ ID NO:X. Thus,

starting with an SEQ ID NO:X, one can use Tables 1, 6 and 7 to determine the corresponding Clone ID, which library it came from and which ATCC deposit the library is contained in. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

[30] In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

[31] A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), the polynucleotide sequence delineated in columns 8 and 9 of Table 2 or the complement thereof, and/or cDNA sequences contained in Clone ID NO:Z (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments, or the cDNA clone within the pool of cDNA clones deposited with the ATCC, described herein), and/or the polynucleotide sequence delineated in column 6 of Table 1B or the complement thereof. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

[32] Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished

through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

[33] Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

[34] Of course, a polynucleotide which hybridizes only to polyA⁺ sequences (such as any 3' terminal polyA⁺ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

[35] The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

[36] The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth. Enzymol. 182:626-646 (1990); Rattan et al., Ann. N.Y. Acad. Sci. 663:48-62 (1992)).

[37] "SEQ ID NO:X" refers to a polynucleotide sequence described, for example, in Tables 1A or 2, while "SEQ ID NO:Y" refers to a polypeptide sequence described in column 6 of Table 1A. SEQ ID NO:X is identified by an integer specified in column 4 of Table 1A. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded

by polynucleotide SEQ ID NO:X. "Clone ID NO:Z" refers to a cDNA clone described in column 2 of Table 1A.

[38] "A polypeptide having functional activity" refers to a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

[39] The PFAM accession number disclosed in Table 2, column 6 provides a link, through publicly accessible databases (see, for example the Sanger Centre PFAM web server at <http://www.sanger.ac.uk/>, and included links to PROSITE, SWISSPROT, GenBank, and other sequence databases), to the associated EC code, or closely-related EC codes. As described above, EC codes provide a description of the biochemical reaction(s) catalyzed by an enzyme family. Based on the associated EC code(s), one can routinely test the polypeptides of the invention for functional activity (e.g. biological activity) using or routinely modifying assays known in the art and/or assays described herein. For example, one of skill in the art may routinely assay enzyme polypeptides (including fragments and variants) of the invention for activity using assays as described in Examples 38, 39, 46, 47, 55, 60, 61, 62, and 65. Many other enzyme assays are known in the art, and may be useful for demonstrating activities of the polypeptides of the present invention.

[40] "A polypeptide having biological activity" refers to a polypeptide exhibiting activity similar to, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).

[41] Table 1A summarizes some of the polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and clones (Clone ID NO:Z) and further

summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby.

Polynucleotides and Polypeptides of the InventionTABLE 1A

| Gene No: | Clone ID NO: Z | Contig ID: | SEQ ID NO: X | ORF (From-To) | AA SEQ ID NO: Y | Predicted Epitopes | Tissue Distribution Library code: count (see Table IV for Library Codes) | Cytologic Band | OMIM Disease Reference(s): |
|----------|----------------|------------|--------------|---------------|-----------------|---|--|----------------|----------------------------|
| 1 | HHMMC14 | 1152250 | 11 | 3 - 1088 | 911 | Gln-67 to Pro-75, Glu-166 to Gly-171, Tyr-216 to Glu-225, Ser-306 to Thr-312, Thr-332 to Thr-338. | AR061: 45, AR089: 12, L0777: 28, H0144: 12, L0748: 10, L0766: 9, H0620: 7, L0750: 7, L0581: 7, L0769: 6, L0774: 6, L0749: 5, L0731: 5, H0318: 4, H0510: 4, H0529: 4, L0771: 4, L0775: 4, L0757: 4, H0556: 3, S0360: 3, H0013: 3, H0599: 3, L0770: 3, L0768: 3, L0652: 3, L0655: 3, L0659: 3, S0374: 3, L0751: 3, L0747: 3, L0758: 3, H0341: 2, S0282: 2, H0661: 2, H0662: 2, H0125: 2, S0358: 2, | | |

| | |
|--|--|
| | H0637: 2, S0278: 2, H0024: 2, H0188: 2, H0292: 2, H0031: 2, S0036: 2, H0264: 2, H0059: 2, H0494: 2, H0509: 2, S0344: 2, L0369: 2, L0761: 2, L0662: 2, L0807: 2, L0666: 2, H0547: 2, S0126: 2, H0435: 2, S0328: 2, S0027: 2, S0032: 2, L0744: 2, L0786: 2, L0593: 2, L0362: 2, H0423: 2, H0624: 1, H0171: 1, T0002: 1, H0583: 1, H0656: 1, S0116: 1, H0255: 1, H0192: 1, S0420: 1, L0005: 1, S0354: 1, S0376: 1, S0410: 1, S0007: 1, S0045: 1, S0046: 1, S0132: 1, H0357: 1, H0455: 1, H0592: 1, H0574: 1, H0492: 1, H0486: 1, T0114: 1, S0280: 1, L0021: 1, H0618: 1, S0010: 1, S0346: 1, S0049: 1, L0040: 1, H0545: 1, H0046: 1, H0150: 1 |
|--|--|

H0246: 1, T0003: 1,
H0373: 1, H0355: 1,
S0628: 1, H0266: 1,
S0334: 1, H0424: 1,
H0417: 1, H0169: 1,
L0455: 1, H0135: 1,
H0163: 1, H0040: 1,
H0087: 1, H0268: 1,
H0413: 1, H0623: 1,
L0351: 1, T0042: 1,
S0438: 1, H0130: 1,
H0646: 1, S0144: 1,
S0142: 1, L0762: 1,
L0796: 1, L0637: 1,
L0374: 1, L0764: 1,
L0773: 1, L0389: 1,
L0806: 1, L0776: 1,
L0657: 1, L0383: 1,
L0382: 1, L0647: 1,
L0663: 1, T0068: 1,
H0520: 1, H0690: 1,
H0683: 1, H0659: 1,
H0658: 1, H0660: 1,
H0672: 1, S0044: 1,
H0134: 1, H0478: 1,
L0754: 1, L0756: 1,
L0779: 1, L0752: 1,
L0753: 1, L0755: 1,
L0759: 1, L0608: 1,
H0668: 1, H0665: 1 and
H0506: 1

| | | | | | | | | | |
|---|---------|---------|-----|------------|------|---|--|--|--|
| 2 | HSLEQ79 | 969371 | 652 | 3 - 1070 | 1552 | Gln-61 to Pro-69, Glu-160 to Gly-165, Tyr-210 to Glu-219, Ser-300 to Thr-306, Thr-326 to Thr-332. | AR061: 3, AR089: 2 S0001: 1, S0390: 1, S0028: 1 and L0592: 1. | | |
| | | 1184946 | 12 | 674 - 3 | 912 | | | | |
| | | 752382 | 653 | 1 - 672 | 1553 | | | | |
| 3 | HUCME08 | 1082023 | 13 | 2 - 595 | 913 | His-29 to Cys-37, Glu-40 to Pro-49, Glu-140 to Gly-145. | H0318: 3, H0656: 2, H0620: 2, S0420: 1, S0045: 1, H0393: 1, H0357: 1, S0346: 1, H0581: 1, S0628: 1, H0539: 1, L0748: 1, L0750: 1 and L0777: 1. | | |
| | | 868780 | 654 | 2 - 676 | 1554 | His-29 to Cys-37, Glu-40 to Pro-49. | | | |
| | | 1152254 | 14 | 520 - 1158 | 914 | Ser-1 to Asp-12, Gln-103 to Cys-108, Ser-173 to Lys-182. | AR089: 1, AR061: 1 S0028: 12, S0045: 5, S0144: 4, S0001: 3, S0044: 3, S0031: 3, S0282: 2, H0597: 2, H0617: 2, S0428: 2, S0390: 2, S0037: 2, S0260: 2, H0624: 1, H0171: 1, H0381: 1, H0346: 1, S0132: 1, S0300: 1, S0278: 1, H0318: 1, H0204: 1, | | |
| 4 | HNGOW33 | 1152254 | 14 | 520 - 1158 | 914 | Ser-1 to Asp-12, Gln-103 to Cys-108, Ser-173 to Lys-182. | AR089: 1, AR061: 1 S0028: 12, S0045: 5, S0144: 4, S0001: 3, S0044: 3, S0031: 3, S0282: 2, H0597: 2, H0617: 2, S0428: 2, S0390: 2, S0037: 2, S0260: 2, H0624: 1, H0171: 1, H0381: 1, H0346: 1, S0132: 1, S0300: 1, S0278: 1, H0318: 1, H0204: 1, | | |

| | | | | | | | | | | | |
|---|---------|-------------------|-----------|-------------------------|-------------|--|--|--|--|--|--|
| | | | | | | | | | S0050: 1, H0271: 1, H0416: 1, H0644: 1, H0181: 1, S0036: 1, H0359: 1, S0150: 1, H0144: 1 and S0146: 1. | | |
| 5 | HT4GD03 | 957351 1103896 | 655 15 | 268 - 1320 153 - 968 | 1555 915 | Ser-1 to Arg-11. Pro-1 to Leu-6, His-25 to Arg-30, Lys-40 to Lys-46, Thr-95 to Asp-100, Gly-125 to Gly-130, Arg-139 to Pro-144, Lys-179 to Met-187. | AR061: 10, AR089: 5 H0585: 37, H0141: 10, L0809: 6, L0794: 5, L0752: 3, H0135: 2, H0494: 2, L0803: 2, L0749: 2, S6024: 1, S0212: 1, H0255: 1, S0356: 1, H0510: 1, L0761: 1, L0772: 1, L0800: 1, L0773: 1, L0766: 1, L0806: 1, L0782: 1, L0788: 1, H0144: 1, H0659: 1, H0187: 1, L0750: 1, L0777: 1 and L0758: 1. | | | | |
| 6 | HAQBZ89 | 923731 949061 | 656 16 | 455 - 967 2 - 325 | 1556 916 | His-14 to Pro-19. Ala-20 to Arg-25. | AR061: 9, AR089: 6 L0659: 4, L0758: 4, L0777: 3, S0360: 2, L0775: 2, L0750: 2, L0731: 2, H0295: 1, S0218: 1, H0255: 1, H0402: 1, L0717: 1, H0411: 1, H0015: 1. | | | | |

| | | | | | | | | | | | | |
|----|---------|--------|----|------------|-----|--|--|--|---|--|--|--|
| | | | | | | | | | H0030: 1, H0644: 1, H0673: 1, H0087: 1, L0770: 1, L0769: 1, L0637: 1, L0761: 1, L0646: 1, L0387: 1, L0766: 1, L0776: 1, L0655: 1, L0789: 1, H0683: 1, S0027: 1, L0748: 1, L0779: 1 and L0757: 1. | | | |
| 7 | HCCCC81 | 949062 | 17 | 139 - 921 | 917 | Gly-8 to Ile-13, Glu-141 to His-146, Glu-186 to Glu-195, Asp-213 to Asn-218. | | | AR089: 12, AR061: 7 H0583: 1, H0675: 1 and H0457: 1. | | | |
| 8 | HE8PW83 | 927532 | 18 | 1 - 546 | 918 | Glu-69 to Gln-76. | | | AR089: 0, AR061: 0 L0748: 6, L0749: 6, L0803: 3, L0774: 3, L0775: 3, H0574: 1, H0632: 1, H0013: 1, L0789: 1, L0790: 1, H0144: 1 and L0581: 1. | | | |
| 9 | HE9QQ22 | 949080 | 19 | 3 - 563 | 919 | | | | AR061: 11, AR089: 3 L0748: 3, H0144: 2, H0632: 1 and L0581: 1. | | | |
| 10 | HFPFB39 | 946170 | 20 | 1613 - 462 | 920 | Pro-36 to Lys-46, Pro-56 to Ala-68, Ala-85 to Arg-90, Tyr-191 to Asn-198, Gly-219 to Val-224, Leu-232 to Lys-238, | | | AR061: 6, AR089: 3 S0010: 4, S0222: 3, H0455: 2, L0803: 2, L0439: 2, L0745: 2, S0282: 1, S0400: 1, H0456: 1, H0441: 1, | | | |

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| 11 | HSDJI44 | 1151680 | 21 | 272 - 2143 | 921 | His-260 to Ala-266. | S0346: 1, H0509: 1, L0769: 1, L0438: 1, L0756: 1 and S0106: 1. AR061: 0, AR089: 0 S0045: 6, H0255: 5, S0028: 4, S0031: 2, S0260: 2, H0341: 1, S0278: 1, H0333: 1, H0250: 1, S0050: 1, H0271: 1, H0100: 1, S0216: 1, S0044: 1 and S0390: 1. | | |
| | | 974784 | 657 | 210 - 1847 | 1557 | Ala-324 to Phe-332, Arg-336 to Thr-343, Pro-373 to Arg-384, Lys-424 to Asp-431. | | | |
| 12 | HE9DG38 | 1181748 | 22 | 2 - 994 | 922 | Ala-30 to Lys-45, Ala-71 to Ala-85, Gly-112 to Asn-117, Asn-131 to Gly-140, Ser-143 to Ala-148, Leu-230 to Val-235, Gly-301 to Asn-312. | AR061: 6, AR089: 2 H0052: 3, H0457: 3, H0618: 2, H0622: 2, L0770: 2, L0438: 2, L0439: 2, H0257: 1, L0471: 1, H0428: 1, H0135: 1, H0144: 1, H0519: 1, H0521: 1, L0741: 1, L0756: 1 and H0707: 1. | | |
| | | 943384 | 658 | 1 - 1371 | 1558 | Ala-28 to Lys-43, Ala-69 to Ala-83, Gly-110 to Asn-115, Asn-129 to Gly-138, | | | |

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| 13 | HGBAT24 | 1024746 | 23 | 1 - 420 | 923 | Ser-141 to Ala-146. | AR061: 41, AR089: 30 H0014: 2, S0028: 1 and S0031: 1. | | |
| 14 | HTDAF92 | 761143 | 659 | 1 - 420 | 1559 | | | | |
| | | 1181747 | 24 | 112 - 1011 | 924 | Leu-71 to Val-76, Gly-142 to Asn-153, Asp-180 to Arg-188, Ser-202 to Asn-212, His-244 to Pro-251, Arg-275 to Ala-280. | AR089: 2, AR061: 1 L0439: 3, S0222: 2, H0543: 2, S0360: 1, H0622: 1, H0063: 1, H0477: 1, T0042: 1, L0369: 1, L0771: 1, L0662: 1, L0659: 1, L0809: 1 and L0786: 1. | | |
| | | 943385 | 660 | 112 - 627 | 1560 | Leu-71 to Val-76, Gly-142 to Asn-153. | | | |
| 15 | HAPSI19 | 972980 | 661 | 718 - 401 | 1561 | Thr-15 to Tyr-20, Ser-54 to Leu-63. | | | |
| | | 668405 | 25 | 176 - 397 | 925 | Leu-1 to Tyr-10. | AR089: 389, AR061: 120 | 19q13.3-q13.4 | 113900, 126340, 126391, 130410, 134790, 138570, 160900, 173850, 191044, 258501, 600040, 600138, 602225, |
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| 16 | HADTU18 | 666268 | 26 | 185 - 442 | 926 | Leu-48 to Gln-54. | AR061: 197, AR089: 100 | | 602225 |
| 17 | HNTEF53 | 954852 | 27 | 33 - 938 | 927 | Pro-45 to Ser-53, Ala-55 to Ala-63, Asp-130 to Leu-136. | AR089: 2, AR061: 1, L0439: 4, L0105: 2, H0271: 2, L0637: 2, L0653: 2, H0519: 2, S0330: 2, H0431: 1, H0052: 1, L0471: 1, H0375: 1, L0763: 1, L0794: 1, L0803: 1, L0774: 1, L0806: 1, L0526: 1, L0809: 1, L0666: 1, L0664: 1 and H0648: 1. | | |
| 18 | HWLLB11 | 954849 | 28 | 51 - 524 | 928 | Pro-1 to Glu-10, His-60 to Arg-76, Pro-79 to Arg-85, Ala-95 to Ile-101, Glu-124 to Glu-130, Lys-151 to Arg-158. | AR061: 2, AR089: 2, S0358: 2, L0657: 1 and L0601: 1. | | |
| 19 | HCRQK86 | 1193068 | 29 | 2 - 1339 | 929 | Arg-1 to Gly-7, Pro-19 to Cys-27, Leu-61 to Ala-72, Ser-90 to Ser-96, Thr-126 to Ser-143, Glu-167 to Gln-176, Ile-185 to Ser-193, Phe-249 to Phe-256, | AR061: 1, AR089: 1, L0748: 6, H0013: 3, L0794: 3, L0438: 3, L0747: 3, L0731: 3, L0005: 2, S0360: 2, H0494: 2, L0769: 2, L0766: 2, L0803: 2, L0655: 2, L0756: 2, | | |

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| | | | | Ala-260 to Ser-271, Tyr-298 to Lys-304, Ser-311 to Arg-322, Ser-346 to Gly-356, Glu-400 to Ser-411. | L0758: 2, H0624: 1, H0170: 1, H0556: 1, H0294: 1, S0116: 1, H0341: 1, H0484: 1, H0638: 1, S0418: 1, S0420: 1, S0356: 1, H0637: 1, H0580: 1, L0717: 1, H0392: 1, H0618: 1, H0052: 1, H0622: 1, H0033: 1, H0553: 1, H0617: 1, H0264: 1, H0272: 1, H0413: 1, S0038: 1, H0100: 1, H0509: 1, S0422: 1, S0426: 1, L0639: 1, L0646: 1, L0800: 1, L0662: 1, L0378: 1, L0636: 1, L0647: 1, L0367: 1, L0789: 1, L0666: 1, H0144: 1, H0682: 1, H0436: 1, L0611: 1, L0779: 1, L0777: 1, L0752: 1, L0753: 1, L0608: 1, L0601: 1 and S0276: 1. |
| 918014 | 662 | 2 - 1324 | 1562 | Pro-14 to Cys-22, Leu-56 to Ala-67, Ser-85 to Ser-91, Thr-121 to Ser-138. | |

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| 20 | HOCOT88 | 933635 | 30 | 331 - 1449 | 930 | Glu-162 to Gln-171, Ile-180 to Ser-188, Phe-244 to Phe-251, Ala-255 to Ser-266, Tyr-293 to Lys-299, Ser-306 to Arg-317, Ser-341 to Gly-351, Glu-395 to Ser-406. Ser-13 to Arg-19, Leu-28 to Val-35, Pro-37 to Gly-57, Ser-81 to Pro-87, Ile-102 to Arg-111. | AR061: 1, AR089: 0 L0766: 3, H0341: 2, H0599: 2, H0457: 2, H0169: 2, S0146: 2, H0444: 2, H0445: 2, L0592: 2, H0619: 1, S0222: 1, H0455: 1, H0592: 1, H0486: 1, H0013: 1, S0010: 1, S0665: 1, H0544: 1, L0471: 1, T0042: 1, H0560: 1, H0359: 1, L0662: 1, L0528: 1, L0529: 1, L0543: 1, L0438: 1, H0435: 1, H0660: 1, H0518: 1, S0044: 1, L0439: 1, L0745: 1, L0753: 1, S0260: 1, L0594: 1, H0542: 1, H0423: 1 and H0422: 1. | | |
| 21 | HEI EE11 | 926930 | 31 | 53 - 695 | 931 | Phe-21 to Lys-27. | AR061: 1, AR089: 1 | | |

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| 22 | HOUGD29 | 1204714 | 32 | 199 - 1821 | 932 | Arg-9 to Gln-17, Ile-33 to Asn-39, Gln-93 to Ser-104, Asp-141 to Leu-155, Ser-224 to Asn-234, Asn-243 to Lys-248, Ser-308 to Gln-320, Thr-350 to Glu-357, Ser-384 to Thr-390, Asp-435 to Ser-447, Ala-480 to Lys-487, Lys-496 to Leu-508, Ser-519 to Val-528, Ser-533 to Gln-541. | S0045: 1 and H0457: 1. AR061: 6, AR089: 5 L0770: 4, L0789: 3, L0439: 3, L0750: 3, L0641: 2, L0747: 2, L0758: 2, S0040: 1, H0575: 1, T0010: 1, H0087: 1, S0422: 1, L0803: 1, L0375: 1, L0776: 1, L0659: 1, L0783: 1, H0144: 1, L0352: 1, H0684: 1, H0660: 1, S0027: 1, L0777: 1 and H0445: 1. | | |
| 23 | HSIGN57 | 910078 | 33 | 199 - 909 2 - 760 | 1563 933 | Arg-9 to Leu-15. Val-10 to Gly-16, Met-19 to Val-34. | AR061: 2, AR089: 1 H0229: 1, H0590: 1, S0049: 1, H0014: 1, H0560: 1, L0439: 1 and H0543: 1. | | |
| 24 | HTEPE35 | 948475 | 34 | 839 - 78 | 934 | Tyr-1 to Lys-8, Phe-19 to Ser-24, Thr-28 to Ser-34, Pro-54 to Trp-70. | AR061: 4, AR089: 1 L0758: 7, L0768: 2, H0616: 1 and L0151: 1. | | |
| 25 | HUFDB74 | 1227205 | 35 | 2 - 562 | 935 | Gln-43 to Thr-58, Asn-74 to His-79, Gly-109 to Trp-114, Asp-136 to Phe-145. | AR061: 1, AR089: 1 H0575: 2, L0754: 2, H0599: 1, T0048: 1, L0163: 1, H0051: 1, H0188: 1, H0379: 1, | | |

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| | | | | | | | | | L0438: 1, H0670: 1, H0672: 1, L0439: 1, L0747: 1, S0260: 1, L0591: 1 and H0506: 1. | | |
| | | 901451 | 664 | 2 - 412 | 1564 | Gln-43 to Thr-58, Asn-74 to His-79, Gly-109 to Trp-114. | | | | | |
| 26 | HBXAB33 | 1229908 | 36 | 3 - 581 | 936 | Asp-1 to Ala-6, Pro-25 to Pro-30. | | | AR089: 8, AR061: 4 L0748: 35, L0747: 15, H0052: 11, L0766: 11, L0439: 10, L0740: 9, L0595: 9, H0556: 8, H0599: 6, S0010: 6, S0418: 5, H0318: 5, H0050: 5, H0673: 5, H0591: 5, L0770: 5, L0593: 5, H0265: 4, S0046: 4, H0431: 4, H0574: 4, H0013: 4, H0083: 4, S0022: 4, L0776: 4, H0144: 4, L0746: 4, L0750: 4, L0777: 4, L0752: 4, L0731: 4, L0604: 4, L0603: 4, S0420: 3, S0354: 3, H0261: 3, H0331: 3, H0156: 3, H0046: 3, H0373: 3, H0266: 3, H0090: 3, H0551: 3, H0413: 3, | | |

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| | | | | | H0561: 3, L0775: 3, L0806: 3, L0509: 3, L0663: 3, H0435: 3, S0152: 3, H0171: 2, S0116: 2, S0376: 2, H0393: 2, L0717: 2, S0222: 2, L0623: 2, T0039: 2, H0024: 2, H0014: 2, T0010: 2, H0288: 2, S0250: 2, S0003: 2, H0031: 2, L0456: 2, H0135: 2, H0038: 2, H0616: 2, S0038: 2, H0560: 2, H0509: 2, H0646: 2, L0769: 2, L0646: 2, L0648: 2, L0662: 2, L0768: 2, L0774: 2, L0651: 2, L0659: 2, L0666: 2, L0664: 2, L0438: 2, S0126: 2, H0539: 2, H0521: 2, S0037: 2, S3014: 2, S0028: 2, L0742: 2, L0756: 2, L0758: 2, L0759: 2, L0596: 2, L0588: 2, L0591: 2, L0592: 2, L0485: 2, L0581: 2, L0599: 2, L0594: 2, S0192: 2, H0542: 2, H0543: 2 |
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| | H0624: 1, S0040: 1, S0114: 1, T0049: 1, H0341: 1, S0001: 1, H0664: 1, H0458: 1, H0125: 1, S0356: 1, S0360: 1, S0045: 1, H0619: 1, S6026: 1, H0351: 1, S0278: 1, H0391: 1, H0409: 1, H0587: 1, H0632: 1, H0244: 1, H0250: 1, H0069: 1, H0575: 1, S0346: 1, S0049: 1, H0597: 1, H0544: 1, H0009: 1, H0178: 1, H0123: 1, L0471: 1, S0362: 1, L0163: 1, N0007: 1, S0051: 1, H0290: 1, S0214: 1, H0428: 1, H0039: 1, H0622: 1, T0006: 1, H0644: 1, H0181: 1, S0364: 1, L0455: 1, S0036: 1, T0067: 1, H0380: 1, H0264: 1, H0488: 1, H0623: 1, H0059: 1, H0494: 1, H0625: 1, S0150: 1, S0344: 1, S0210: 1, S0002: 1, S0426: 1, L0371: 1, L0761: 1, |
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| 27 | HMABF84 | 1198479 | 957228 | 665 | 2424 - 1081 | 1565 | Lys-70 to Met-78, Tyr-85 to Lys-91, Gln-195 to Cys-205, Pro-234 to Lys-245, Gly-270 to Asp-275, Asp-315 to Ser-324, Pro-352 to Gln-357, Leu-380 to Trp-389. | L0642: 1, L0764: 1, L0771: 1, L0498: 1, L0497: 1, L0804: 1, L0542: 1, L0782: 1, L0383: 1, L0809: 1, L0647: 1, L0665: 1, S0374: 1, H0547: 1, H0519: 1, H0690: 1, H0670: 1, H0660: 1, H0134: 1, S0432: 1, L0755: 1, S0031: 1, L0608: 1, L0366: 1, S0011: 1 and S0026: 1. | |
| | | | | | | | Pro-21 to Arg-28, Arg-56 to Thr-63, Tyr-84 to Asp-89. | AR061: 3, AR089: 1 H0617: 4, S0212: 2, S0360: 2, S0144: 2, L0803: 2, H0587: 1, H0013: 1, H0046: 1, H0616: 1, H0100: 1, S0422: 1, H0529: 1, L0774: 1, L0809: 1, L0790: 1, L0791: 1. | |

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| | | | | | | | | L0748: 1 and L0747: 1. | | |
| | | 944629 | 666 | 1 - 465 | 1566 | | Arg-14 to Thr-21, Tyr-42 to Asp-47. | | | |
| 28 | HPTVF17 | 1150836 | 38 | 712 - 245 | 938 | | Gly-1 to Gln-11, Ser-24 to Cys-33, Thr-37 to Gly-46, Thr-51 to Thr-63. Pro-10 to Pro-17, Cys-41 to Pro-50, Asn-64 to Arg-73, Ser-81 to Arg-87, Glu-93 to Pro-100. | AR061: 8, AR089: 4 H0424: 1 and L0595: 1. | | |
| | | 936688 | 667 | 2 - 679 | 1567 | | | | | |
| 29 | HSDIC55 | 1197407 | 39 | 570 - 1 | 939 | | Leu-29 to Gly-40, Tyr-93 to Ile-100. Tyr-28 to Val-37, Gln-39 to Met-44, Leu-52 to Asp-60. | AR089: 0, AR061: 0 | | |
| | | 506582 | 668 | 1 - 381 | 1568 | | | | | |
| 30 | HSDIL35 | 1228138 | 40 | 2 - 313 | 940 | | | AR089: 1, AR061: 0 H0598: 1, S0028: 1 and S0260: 1. | | |
| | | 656370 | 669 | 3 - 371 | 1569 | | | | | |
| 31 | HTXSM05 | 1104951 | 41 | 2 - 565 | 941 | | Pro-48 to Gly-53, Pro-88 to Ser-94, Gly-103 to Ser-108, Pro-141 to Gln-150. Pro-48 to Gly-53, Pro-88 to Ser-94, Gly-103 to Gly-111. | AR061: 10, AR089: 5 H0264: 2, H0556: 1, S0366: 1, S3012: 1 and L0485: 1. | | |
| | | 958447 | 670 | 2 - 424 | 1570 | | | | | |
| 32 | HYAAH23 | 1032585 | 42 | 322 - 606 | 942 | | Ser-39 to Thr-45, Thr-65 to Thr-71. | AR061: 23, AR089: 15 L0777: 28, H0257: 19, | 9q12 | 602014 |

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| | | | | H0144: 12, L0748: 10, L0766: 9, H0620: 7, L0769: 7, L0750: 7, L0581: 7, H0559: 6, L0774: 6, L0749: 6, H0529: 5, L0771: 5, L0751: 5, L0731: 5, L0757: 5, H0318: 4, H0510: 4, L0775: 4, L0744: 4, H0556: 3, S0360: 3, H0256: 3, H0013: 3, H0599: 3, H0266: 3, H0059: 3, L0770: 3, L0662: 3, L0768: 3, L0652: 3, L0655: 3, L0659: 3, L0666: 3, S0374: 3, L0747: 3, L0758: 3, L0595: 3, H0341: 2, S0282: 2, H0661: 2, H0662: 2, H0125: 2, S0358: 2, H0637: 2, S0278: 2, H0024: 2, H0373: 2, H0188: 2, H0292: 2, H0031: 2, S0036: 2, H0264: 2, H0494: 2, H0509: 2, S0144: 2, S0344: 2, L0369: 2, L0761: 2, L0807: 2, L0663: 2, H0547: 2, S0126: 2. |
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| | H0435: 2, S0328: 2, S0027: 2, S0032: 2, L0786: 2, L0593: 2, L0362: 2, H0423: 2, H0624: 1, H0171: 1, T0002: 1, S0134: 1, H0583: 1, H0656: 1, S0116: 1, S0212: 1, H0255: 1, H0192: 1, S0420: 1, L0005: 1, S0354: 1, S0376: 1, S0410: 1, S0007: 1, S0045: 1, S0046: 1, S0132: 1, H0440: 1, L0717: 1, H0357: 1, H0455: 1, H0592: 1, H0333: 1, H0574: 1, H0492: 1, H0486: 1, T0114: 1, S0280: 1, L0021: 1, H0575: 1, H0618: 1, S0010: 1, S0346: 1, S0049: 1, H0196: 1, L0040: 1, H0545: 1, H0046: 1, H0150: 1, H0123: 1, H0246: 1, T0003: 1, H0355: 1, S6028: 1, S0334: 1, H0252: 1, H0424: 1, H0417: 1, H0169: 1, L0455: 1, H0135: 1, H0163: 1, | |
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| H0040: 1, H0087: 1, H0268: 1, H0413: 1, H0623: 1, L0351: 1, T0042: 1, S0438: 1, H0130: 1, H0646: 1, S0142: 1, S0002: 1, L0762: 1, L0796: 1, L0637: 1, L0800: 1, L0374: 1, L0764: 1, L0773: 1, L0767: 1, L0794: 1, L0389: 1, L0806: 1, L0776: 1, L0657: 1, L0658: 1, L0383: 1, L0382: 1, L0647: 1, L0789: 1, L0664: 1, L0565: 1, T0068: 1, H0520: 1, H0690: 1, H0683: 1, H0659: 1, H0658: 1, H0660: 1, H0672: 1, H0651: 1, H0521: 1, S0044: 1, H0134: 1, H0478: 1, L0439: 1, L0754: 1, L0756: 1, L0779: 1, L0752: 1, L0753: 1, L0755: 1, L0759: 1, L0608: 1, H0668: 1, H0665: 1, S0276: 1, S0196: 1, H0506: 1 and H0352: 1. | | | | | | |
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| 33 | HTPDX13 | 1134372 | 43 | 2 - 922 | 943 | | AR089: 0, AR061: 0 H0549: 1, H0485: 1, H0039: 1, H0553: 1, H0040: 1 and S0126: 1. | | |
| | | 948419 | 671 | 2 - 922 | 1571 | | | | |
| 34 | HAIHE43 | 1172244 | 44 | 2 - 376 | 944 | | AR089: 20, AR061: 8 H0599: 2, L0759: 2, H0556: 1, H0638: 1, S0418: 1, S6022: 1, L0021: 1, S0010: 1, H0266: 1, H0553: 1, H0644: 1, L0763: 1, L0641: 1, L0766: 1, L0805: 1, L0655: 1, H0539: 1, S0028: 1 and L0777: 1. | | |
| | | 966830 | 672 | 2 - 376 | 1572 | | | | |
| 35 | HAIJAV28 | 948630 | 45 | 3 - 464 | 945 | Pro-1 to Ala-12. | AR089: 3, AR061: 1 L0747: 12, L0755: 12, L0766: 9, L0438: 9, L0754: 7, H0046: 6, L0751: 6, L0752: 6, H0068: 5, L0775: 5, L0439: 5, S0010: 4, H0547: 4, S0152: 4, L0740: 4, L0779: 4, L0759: 4, H0591: 3, L0771: 3, L0662: 3, L0774: 3, L0666: 3, S0028: 3, L0748: 3, | 1q21-q25 | 104770, 107300, 107670, 110700, 131210, 135940, 136132, 145001, 146790, 150292, 152445, 152445, 159001, |

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| L0756: 3, L0731: 3, L0757: 3, H0624: 2, S0045: 2, H0619: 2, S0222: 2, S0049: 2, H0052: 2, H0615: 2, S0036: 2, T0041: 2, H0509: 2, S0002: 2, S0426: 2, L0769: 2, L0776: 2, L0659: 2, H0521: 2, H0707: 2, L0594: 2, L0362: 2, S0011: 2, H0170: 1, H0171: 1, H0685: 1, S0040: 1, T0049: 1, H0657: 1, S0001: 1, H0638: 1, S0358: 1, S0360: 1, S0408: 1, H0637: 1, S0007: 1, S0132: 1, S6022: 1, H0550: 1, H0431: 1, H0455: 1, H0574: 1, H0486: 1, T0114: 1, H0250: 1, H0069: 1, H0156: 1, L0105: 1, H0597: 1, H0546: 1, H0545: 1, H0050: 1, L0163: 1, H0594: 1, H0266: 1, H0290: 1, S0214: 1, H0328: 1, H0688: 1, H0622: 1, H0032: 1, H0673: 1, | 173610, 174000, 179755, 182860, 182860, 182860, 191315, 208250, 230800, 230800, 233710, 266200, 600897, 600995, 601105, 601412, 601518, 601652, 602491 |
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| 36 | HAPOR59 | 712955 | 46 | 3 - 368 | 946 | Ala-4 to Glu-11, Lys-62 to Arg-71. | AR089: 29, AR061: 9 H0575: 1 and H0083: 1. | | | | | | |
| 37 | HBIBF78 | 1123470 | 47 | 879 - 640 | 947 | | AR061: 6, AR089: 3 S0049: 1 and L0439: 1. | | | | | | |
| | | 772797 | 673 | 45 - 206 | 1573 | Lys-42 to Ser-49. | | | | | | | |
| 38 | HCDAJ15 | 1091635 | 48 | 176 - 388 | 948 | Arg-12 to Thr-20, | AR089: 8, AR061: 8 | | | | | | |

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| | | | | | | | His-55 to Lys-61. | | | H0251: 2 and S0392: 1. | | |
| | | 557243 | 674 | 2 - 190 | 1574 | | | | | | | |
| 39 | HCE1S21 | 671209 | 49 | 1 - 297 | 949 | | Glu-9 to Asp-14. | | | AR061: 5, AR089: 2 H0052: 1, L0581: 1 and L0366: 1. | | |
| 40 | HCE3J64 | 951228 | 50 | 3 - 593 | 950 | | Thr-1 to Lys-8, Lys-26 to Asp-33, Gln-60 to Trp-70, Phe-99 to Lys-106, Asp-126 to Asn-137, Arg-139 to Glu-145, Met-157 to Tyr-164, Asn-167 to Arg-174. | | | AR089: 24, AR061: 15 H0052: 2, L0759: 2, S0376: 1, H0333: 1, S0388: 1, L0637: 1, L0636: 1, L0742: 1 and L0439: 1. | | |
| 41 | HCFCV92 | 1124565 | 51 | 922 - 1143 | 951 | | Gly-68 to Leu-74. | | | AR089: 2, AR061: 2 L0766: 3, H0521: 2, H0422: 2, H0661: 1, H0369: 1, H0687: 1, L0646: 1, L0655: 1, L0665: 1, H0519: 1, H0436: 1 and L0779: 1. | | |
| 42 | HCFLI54 | 934216 | 675 | 413 - 655 | 1575 | | | | | AR089: 1, AR061: 0 L0439: 6, L0748: 5, L0758: 4, L0591: 4, L0766: 3, L0805: 3, L0438: 3, H0102: 2, L0666: 2, L0740: 2, H0423: 2, S0360: 1, S0046: 1, H0393: 1, H0411: 1, H0391: 1, | | |
| | | 921382 | 52 | 259 - 522 | 952 | | | | | | | |

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| 43 | HCFND04 | 1155680 | 53 | 1 - 1146 | 953 | Pro-2 to Leu-23, Gln-54 to Gly-62, Glu-68 to Asn-80, Glu-82 to Pro-94, Gln-100 to Thr-108, Pro-114 to Lys-123, Pro-128 to Lys-137, Leu-143 to Lys-151, Pro-157 to Gly-170, Lys-173 to Lys-185, Asp-193 to Glu-211, Gly-236 to Met-241, Asp-298 to Trp-304, Tyr-306 to Ile-314, Thr-322 to Tyr-331, Thr-371 to Thr-376. | AR089: 7, AR061: 3 S0474: 1, T0067: 1, L0805: 1, L0777: 1, L0780: 1 and H0423: 1. | H0586: 1, H0156: 1, H0575: 1, H0023: 1, H0266: 1, H0267: 1, H0622: 1, T0006: 1, H0674: 1, S0386: 1, L0770: 1, L0638: 1, L0373: 1, L0662: 1, L0776: 1, L0518: 1, L0809: 1, L0663: 1, H0684: 1, H0435: 1, H0648: 1, H0672: 1, H0436: 1, H0478: 1, L0744: 1 and L0747: 1. | | |
| | | 873441 | 676 | 273 - 1145 | 1576 | Ile-10 to Cys-21, | | | | |

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|----|---------|---------|----|---------|-----|---|---|
| 44 | HCHMV63 | 1190101 | 54 | 889 - 2 | 954 | Thr-24 to Gln-60. Gly-1 to Trp-6, Pro-9 to Asp-18, Val-56 to Thr-66, Pro-73 to Trp-79, Ala-82 to Trp-102, Gln-108 to Cys-119, Ser-145 to Arg-166, Arg-239 to Asn-247. | AR089: 2, AR061: 1 S0412: 12, L0758: 5, L0743: 4, L0748: 4, H0545: 3, L0769: 3, L0665: 3, H0341: 2, S0360: 2, H0457: 2, H0644: 2, H0032: 2, S0144: 2, L0762: 2, L0766: 2, L0774: 2, L0530: 2, H0436: 2, L0747: 2, L0759: 2, L0581: 2, H0352: 2, H0657: 1, H0656: 1, S0282: 1, H0484: 1, H0663: 1, S0358: 1, H0370: 1, L0586: 1, H0013: 1, S0010: 1, H0596: 1, H0594: 1, H0606: 1, H0135: 1, H0090: 1, H0616: 1, H0641: 1, H0633: 1, L0770: 1, L0771: 1, L0662: 1, L0767: 1, L0768: 1, L0803: 1, L0805: 1, L0509: 1, L0653: 1, L0515: 1, L0659: 1, H0520: 1, H0435: 1, H0659: 1, H0521: 1, H0696: 1, |
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| | | | | | | | | | S3014: 1, S0027: 1, L0439: 1, L0740: 1, L0749: 1, L0756: 1, S0260: 1 and H0423: 1. | | |
| 45 | HCWDL45 | 666798 | 677 | 2 - 262 | 1577 | His-48 to Thr-54. | | | AR089: 16, AR061: 4 H0305: 6 and S0052: 1. | | |
| 46 | HCWEI19 | 889416 | 55 | 118 - 282 | 955 | Ala-33 to Ile-42. | | | AR089: 4, AR061: 2 H0305: 2 | | |
| | | 1125258 | 56 | 116 - 448 | 956 | Lys-1 to Ser-7, Pro-71 to Gly-81. | | | | | |
| | | 948690 | 678 | 178 - 309 | 1578 | | | | | | |
| 47 | HCWKB72 | 1224131 | 57 | 1527 - 3206 | 957 | Leu-73 to Lys-87, Met-91 to Pro-171, Glu-198 to Ser-298, Ser-306 to Ser-336, Ser-338 to Ser-373, Pro-379 to Val-407, Ser-410 to Gly-418, Ser-425 to His-458, Val-464 to Arg-541. | | | AR061: 2, AR089: 2 H0305: 4, H0266: 3, H0624: 2, H0618: 2, S0036: 2, H0040: 2, T0041: 2, L0749: 2, L0777: 2, H0265: 1, H0556: 1, S0134: 1, H0013: 1, H0069: 1, H0599: 1, H0575: 1, H0421: 1, T0110: 1, H0188: 1, H0428: 1, H0135: 1, H0634: 1, H0488: 1, H0056: 1, H0623: 1, S0038: 1, S0386: 1, H0100: 1, T0042: 1, L0766: 1, H0521: 1, H0522: 1, H0436: 1, S3014: 1, S0027: 1, L0779: 1, S0260: 1, L0588: 1, | | |

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| 48 | HDDAF49 | 676007 1125713 | 679 58 | 101 - 193 549 - 298 | 1579 958 | | | AR061: 9, AR089: 3 H0339: 1 | | |
| 49 | HDPGQ74 | 911314 691163 | 680 59 | 144 - 320 3 - 320 | 1580 959 | Glu-15 to Ser-24. Asp-19 to Leu-24. | | AR061: 0, AR089: 0 H0551: 5, H0545: 4, H0521: 4, L0748: 4, L0790: 3, S0278: 2, H0586: 2, H0333: 2, H0632: 2, H0052: 2, H0023: 2, S0250: 2, S0142: 2, S0426: 2, H0529: 2, L0565: 2, H0547: 2, L0439: 2, H0170: 1, H0685: 1, H0295: 1, H0458: 1, S0418: 1, L0534: 1, S0132: 1, H0587: 1, H0485: 1, H0544: 1, H0081: 1, L0471: 1, S0050: 1, S0388: 1, H0510: 1, H0286: 1, H0428: 1, H0032: 1, H0124: 1, H0488: 1, L0065: 1, H0538: 1, S0002: 1, L0770: 1, L0769: 1, L0646: 1, L0644: 1, L0773: 1, L0363: 1, L0774: 1. | | |

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| 51 | HDP1X67 | 1172240 | 61 | 3 - 470 | 961 | Gln-19 to Gly-24, Gln-34 to Leu-42, Gln-44 to Gln-49 | AR089: 3, AR061: 1 L0756: 3, H0622: 2, L0751: 2, H0624: 1 | | | |
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| | | | | | | | Gln-56 to Glu-61, Leu-76 to Phe-85, Cys-97 to Arg-102. | | | | H0265: 1, S0402: 1, H0650: 1, S0444: 1, H0497: 1, H0643: 1, H0632: 1, H0673: 1, H0038: 1, H0646: 1, S0002: 1, L0764: 1, L0766: 1, L0803: 1, L0776: 1, L0790: 1, L0666: 1, H0520: 1, S0152: 1, H0521: 1, H0134: 1, L0743: 1, L0777: 1 and H0543: 1. | |
| 52 | HDPXN01 | | 954385 | 681 | 2 - 334 | 1581 | Gln-11 to Glu-16, Leu-31 to Phe-40. | | | | AR089: 9, AR061: 4 L0794: 5, L0439: 2, L0747: 2, H0521: 1, L0779: 1, L0777: 1 and L0594: 1. | |
| 53 | HDQFT77 | | 915919 1136137 | 682 63 | 69 - 230 2 - 958 | 1582 963 | Ser-48 to Ser-53. Pro-13 to Leu-23, Glu-39 to Gly-51, Ser-54 to Glu-65, Ala-77 to Gly-84, Gln-90 to Val-96, Arg-104 to Gly-113, Thr-120 to Cys-125, Asn-154 to Ser-160, Glu-162 to Val-168, Leu-247 to Gln-252, | | | | AR089: 16, AR061: 8 L0803: 5, L0655: 3, L0747: 3, L0779: 3, L0771: 2, L0766: 2, L0775: 2, L0666: 2, S0126: 2, L0755: 2, L0758: 2, H0656: 1, H0351: 1, H0586: 1, H0559: 1, H0598: 1, H0038: 1, L0761: 1, | |

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| 54 | HE2FR50 | 508498 | 64 | 50 - 391 | 964 | <p>Phe-286 to Arg-294, Pro-296 to Tyr-301, Asp-308 to Ser-317.</p> <p>Glu-11 to Gly-23, Ser-26 to Glu-37, Ala-49 to Gly-56, Gln-62 to Val-68, Arg-76 to Gly-85, Thr-92 to Cys-97, Asn-126 to Ser-132, Glu-134 to Val-140, Leu-219 to Gln-224, Phe-258 to Arg-266, Pro-268 to Tyr-273, Asp-280 to Ser-289.</p> | <p>L0804: 1, L0774: 1, L0805: 1, H0521: 1, L0750: 1 and L0759: 1.</p> <p>AR061: 10, AR089: 3 L0659: 3, L0766: 2, S0330: 2, L0731: 2, L0758: 2, H0171: 1, H0650: 1, S0356: 1, H0675: 1, S0182: 1, H0184: 1, H0009: 1, H0039: 1, H0038: 1, H0560: 1, L0770: 1, L0637: 1, L0655: 1, L0666: 1, H0659: 1, S0328: 1, H0518: 1, H0521: 1, L0752: 1, S0260: 1 and L0588: 1.</p> | | |
| 55 | HE2SN25 | 1151226 | 65 | 1239 - 1024 | 965 | Leu-7 to Lys-13. | AR061: 4, AR089: 3 | | |

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| | | | | | | | | | L0439: 2, H0624: 1, H0171: 1, S0114: 1, L0774: 1, H0539: 1 and L0752: 1. | | |
| 56 | HE8AE26 | 948687 1147168 | 684 66 | 134 - 277 247 - 597 | 1584 966 | Thr-1 to His-10. Ser-74 to Ala-81. | | | AR089: 11, AR061: 10 H0013: 2 and H0427: 1. | | |
| | | 851514 | 685 | 34 - 210 | 1585 | | | | | | |
| 57 | HEBGK01 | 963673 | 67 | 453 - 109 | 967 | Gly-48 to Gly-54. | | | AR061: 0, AR089: 0 H0617: 7, H0483: 1, S0007: 1, S0051: 1, H0182: 1, H0606: 1, L0769: 1, L0761: 1 and H0547: 1. | | |
| 58 | HEFMB30 | 691516 | 68 | 51 - 221 | 968 | | | | AR061: 1, AR089: 0 L0804: 2, S0402: 1, H0648: 1, L0748: 1 and L0749: 1. | | |
| 59 | HEOPE58 | 851009 | 69 | 257 - 421 | 969 | Phe-28 to Val-36, Phe-44 to Pro-49. | | | AR089: 1, AR061: 0 H0457: 4 | | |
| 60 | HETBR74 | 948667 | 70 | 216 - 479 | 970 | Leu-78 to Cys-88. | | | AR061: 8, AR089: 6 H0170: 1, S0045: 1, H0619: 1, H0046: 1, L0761: 1, L0754: 1 and S0026: 1. | | |
| 61 | HFCAG94 | 1111177 | 71 | 1010 - 669 | 971 | | | | AR089: 16, AR061: 7 H0009: 1 and H0520: 1. | | |
| | | 735763 | 686 | 82 - 180 | 1586 | | | | | | |

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| 62 | HFPHR82 | 957528 | 72 | 1592 - 273 | 972 | Ile-256 to Val-269, Gln-296 to Gln-301, Ile-316 to Leu-322, Glu-351 to Leu-359, Ser-395 to Arg-406, Gly-425 to Leu-431. | AR089: 3, AR061: 1 L0747: 12, L0755: 12, L0766: 9, L0438: 9, L0754: 7, H0046: 6, L0751: 6, L0752: 6, H0068: 5, L0775: 5, L0439: 5, S0010: 4, H0547: 4, S0152: 4, L0740: 4, L0779: 4, L0759: 4, H0591: 3, L0771: 3, L0662: 3, L0774: 3, L0666: 3, S0028: 3, L0748: 3, L0756: 3, L0731: 3, L0757: 3, H0624: 2, S0045: 2, H0619: 2, S0222: 2, S0049: 2, H0052: 2, H0615: 2, S0036: 2, T0041: 2, H0509: 2, S0002: 2, S0426: 2, L0769: 2, L0776: 2, L0659: 2, H0521: 2, H0707: 2, L0594: 2, L0362: 2, S0011: 2, H0170: 1, H0171: 1, H0685: 1, S0040: 1, T0049: 1, H0657: 1, S0001: 1, H0638: 1, S0358: 1, S0360: 1, S0408: 1, H0637: 1, S0007: 1, | 11q21-q25 | 104770, 107300, 107670, 110700, 131210, 135940, 136132, 145001, 146790, 150292, 152445, 152445, 159001, 173610, 174000, 179755, 182860, 182860, 182860, 191315, 208250, 230800, 230800, 233710, 266200, 600897, 600995, 601105, 601412, 601518, 601652, |
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| 63 | HHFO084 | 857780 | 73 | 78 - 275 | 973 | | | | AR089: 7, AR061: 4 S0344: 3, H0539: 2, L0758: 2, H0685: 1, H0657: 1, H0656: 1, S0116: 1, H0341: 1, H0645: 1, H0549: 1, H0331: 1, H0574: 1, T0039: 1, H0318: 1, H0050: 1, H0135: 1, H0641: 1, L0374: 1, L0662: 1, L0768: 1, L0803: 1, L0775: 1, L0776: 1, L0368: 1, L0665: 1, H0689: 1, H0435: 1, H0659: 1, H0134: 1, L0749: 1, L0779: 1, L0759: 1 and S0194: 1. | | | |
| 64 | HISAM68 | 1125189 | 74 | 590 - 3 | 974 | Arg-9 to Leu-28, Ser-108 to Thr-113, Gly-152 to Gly-159, Pro-170 to Ser-184. | | | AR089: 1, AR061: 0 L0803: 6, L0774: 2, H0056: 1, L0761: 1, L0800: 1, L0766: 1, L0806: 1 and H0539: 1. | | | |
| | | 868785 | 687 | 1 - 498 | 1587 | Ser-84 to Thr-89, Gly-128 to Gly-135. | | | | | | |

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| 65 | HLHDD45 | 942901 | 75 | 21 - 230 | 975 | Pro-146 to Ser-160. Lys-1 to Gly-9, Ser-30 to Gly-36. | AR089: 33, AR061: 7 H0556: 3, H0208: 3, H0619: 3, H0050: 3, L0471: 3, H0179: 3, H0644: 3, S0344: 3, H0521: 3, L0439: 3, S0420: 2, S0360: 2, H0599: 2, H0264: 2, H0280: 2, S0210: 2, H0547: 2, H0658: 2, L0750: 2, L0731: 2, L0588: 2, L0604: 2, H0543: 2, H0265: 1, T0002: 1, H0140: 1, S0114: 1, H0341: 1, S0001: 1, H0669: 1, H0662: 1, H0306: 1, S0418: 1, H0580: 1, L0717: 1, H0549: 1, H0453: 1, H0592: 1, H0497: 1, H0632: 1, T0039: 1, T0112: 1, H0575: 1, H0036: 1, H0309: 1, H0544: 1, H0172: 1, H0123: 1, H0620: 1, H0024: 1, H0051: 1, H0188: 1, H0615: 1, H0604: 1, H0031: 1, L0456: 1, | | |
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| 66 | HMMAB49 | 1087684 | 76 | 462 - 160 | 976 | Lys-8 to Ser-13, Lys-52 to Ser-69, Cys-87 to His-93. | | AR089: 53, AR061: 4 H0444: 2 | | | |
| | | 462502 | 688 | 1 - 204 | 1588 | | | | | | |
| 67 | HMSGO27 | 683031 | 77 | 236 - 3 | 977 | Leu-20 to Gly-25, Pro-28 to His-40. | | AR089: 11, AR051: 7, AR061: 1, AR054: 0 H0638: 1, H0046: 1, S0112: 1 and S0002: 1. | | | |
| | | 943946 | 689 | 127 - 462 | 1589 | Ser-1 to Leu-6, His-54 to Cys-61. | | | | | |
| | | 947911 | 690 | 55 - 171 | 1590 | Phe-1 to Arg-12. | | | | | |
| 68 | HNHAM52 | 1125710 | 78 | 880 - 539 | 978 | | | AR061: 2, AR089: 1 | | | |

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| | | | | | | | | | H0457: 1, H0674: 1, L0803: 1, S0053: 1, L0756: 1 and L0592: 1. | | |
| 69 | HNHEQ86 | 457010 | 691 | 12 - 131 | 1591 | Arg-1 to Asp-6, Glu-26 to Ser-33. | | | AR061: 0, AR089: 0 S6024: 1, S0001: 1, S0053: 1, S0216: 1, S0028: 1 and S0260: 1. | | |
| 70 | HNHHF46 | 1123883 | 80 | 1348 - 1040 | 980 | | | | AR061: 4, AR089: 4 L0748: 7, L0774: 2, S0216: 2, L0749: 2, H0455: 1, S0038: 1, S0464: 1, L0637: 1, L0804: 1, L0789: 1 and S0053: 1. | | |
| 71 | HOECV83 | 859822 | 692 | 3 - 284 | 1592 | | | | AR061: 3, AR089: 2 S0354: 2, L0438: 2, L0750: 2, L0586: 1, H0581: 1, H0052: 1, H0009: 1, L0471: 1, L0179: 1, S0003: 1, L0055: 1, L0655: 1, L0526: 1, S0126: 1, H0521: 1 and S0424: 1. | | |
| | | 1123893 | 81 | 1076 - 1456 | 981 | Pro-53 to Glu-63, Ser-105 to Glu-111. | | | | | |
| 72 | HORBO54 | 653276 | 693 | 198 - 389 | 1593 | | | | AR061: 4, AR089: 2 L0758: 4, H0556: 3, H0657: 3, H0435: 3, | | |
| | | 870674 | 82 | 115 - 549 | 982 | | | | | | |

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| 73 | HOSFZ73 | 1122896 | 83 | 182 - 3 | 983 | Glu-41 to Arg-47. | L0596: 1, L0595: 1, H0542: 1, H0423: 1 and S0424: 1. AR089: 74, AR061: 10 S0027: 5, S0356: 2, H0561: 2, L0662: 2, H0659: 2, L0591: 2, H0543: 2, S0282: 1, S0354: 1, H0619: 1, H0575: 1, S0010: 1, S0214: 1, H0674: 1, L0455: 1, H0494: 1, S0142: 1, L0667: 1, L0803: 1, L0805: 1, L0666: 1, L0663: 1, L0664: 1, H0539: 1, H0521: 1, H0436: 1, H0478: 1, H0631: 1, L0755: 1 and S0260: 1. | | |
| 74 | HPIAU71 | 913876 1123830 | 694 84 | 233 - 370 306 - 776 | 1594 984 | Ser-111 to Ala-121. | AR089: 1, AR061: 1 S0150: 2, S3014: 1 and S0028: 1. | | |
| 75 | HRDBT72 | 786811 1112136 507847 | 695 85 696 | 55 - 333 860 - 576 226 - 354 | 1595 985 1596 | Phe-36 to Ser-54, Ala-64 to Asn-70. | AR089: 49, AR061: 16 H0124: 3 | | |
| 76 | HSDFT51 | 1124582 | 86 | 1369 - 812 | 986 | Ala-155 to Gln-160, Arg-166 to Gln-175. | AR061: 6, AR089: 3 L0618: 1, L0770: 1, | | |

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| | | | | | | | L0803: 1 and S0031: 1. | | |
| | | 947918 | 697 | 1 - 591 | 1597 | Ala-155 to Glu-160. | | | |
| 77 | HSDIM56 | 948669 | 87 | 3 - 755 | 987 | Val-174 to Pro-179, Pro-192 to Ile-207. | AR089: 1, AR061: 1 S0028: 3, S0428: 2, S0282: 1, S0045: 1, S0132: 1, S0222: 1, H0416: 1, S0052: 1, S0152: 1 and S0260: 1. | | |
| 78 | HSICX21 | 531267 | 88 | 223 - 378 | 988 | Asn-5 to His-12. | AR089: 2, AR061: 0 H0036: 2 | | |
| 79 | HSIDS82 | 531248 | 89 | 146 - 301 | 989 | His-28 to Gln-36. | AR061: 6, AR089: 3 H0036: 2, H0619: 1, H0050: 1 and L0792: 1. | | |
| 80 | HSNAH21 | 571314 | 90 | 64 - 249 | 990 | Ser-2 to Arg-7, Arg-22 to Pro-28. | AR061: 3, AR089: 1 L0659: 7, L0777: 7, S0358: 6, H0486: 6, H0622: 6, S0360: 4, L0662: 4, H0013: 3, H0144: 3, S0328: 3, L0751: 3, L0731: 3, H0624: 2, H0619: 2, H0328: 2, H0163: 2, L0520: 2, L0764: 2, L0747: 2, S0116: 1, S0356: 1, S0376: 1, H0431: 1, H0600: 1, H0632: 1, H0244: 1, H0599: 1, H0123: 1, H0050: 1, H0051: 1, S0250: 1, H0688: 1, | | |

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| 81 | HSODC08 | 966264 | 91 | 1334 - 222 | 991 | Gln-36 to Asp-41, Ser-73 to Glu-82, Phe-85 to Arg-98, Leu-170 to Glu-176, Lys-226 to Asp-239, Gly-285 to Leu-297, Asp-327 to Glu-339, Glu-343 to Leu-348. | H0039: 1, H0090: 1, H0591: 1, H0040: 1, H0102: 1, S0150: 1, H0647: 1, H0646: 1, L0640: 1, L0763: 1, L0768: 1, L0649: 1, L0806: 1, L0793: 1, L0666: 1, H0690: 1, H0684: 1, H0658: 1, H0648: 1, L0779: 1, L0780: 1, L0759: 1 and S0011: 1. | | |
| | | | | | | | AR089: 5, AR061: 1 H0038: 5, L0748: 5, L0777: 5, L0766: 4, L0769: 3, L0756: 3, L0759: 3, S6028: 2, H0271: 2, L0776: 2, H0435: 2, L0754: 2, L0747: 2, L0779: 2, L0752: 2, L0758: 2, H0595: 2, L0596: 2, H0393: 1, H0431: 1, H0486: 1, H0427: 1, H0004: 1, H0318: 1, H0085: 1, H0546: 1, L0471: 1, S0022: 1, H0252: 1, H0644: 1, H0673: 1, H0674: 1, H0124: 1, H0616: 1, | | |

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| | | | | | | | | S0142: 1, S0422: 1, L0770: 1, L0761: 1, L0771: 1, L0775: 1, L0653: 1, L0634: 1, L0659: 1, L0544: 1, L0664: 1, H0144: 1, S0126: 1, H0670: 1, H0555: 1, H0436: 1, H0627: 1, S0028: 1, L0780: 1, L0731: 1, L0757: 1, L0361: 1, S0026: 1, S0412: 1 and L0697: 1. | | | |
| 82 | HSPAB58 | 736098 | 92 | 3 - 116 | 992 | Ser-20 to Tyr-25. | | AR089: 1, AR061: 0 H0478: 1, L0748: 1 and L0749: 1. | | | |
| 83 | HSQCM85 | 963554 | 93 | 184 - 444 | 993 | | | AR050: 19, AR054: 9, AR051: 5, AR089: 1, AR061: 0 S0216: 1 and S0026: 1. | | | |
| 84 | HTOIA82 | 844319 | 94 | 41 - 286 | 994 | Arg-44 to Gly-59. | | AR061: 4, AR089: 2 H0264: 1 and L0754: 1. | | | |
| 85 | HUUDH57 | 931155 | 95 | 2 - 2167 | 995 | Pro-52 to Thr-58, Pro-115 to Asp-122, Asp-190 to Ile-208. | | AR089: 11, AR061: 1 H0543: 4, S0354: 3, H0423: 3, H0656: 2, L0749: 2, H0306: 1, H0638: 1, S0356: 1, S0358: 1, S0360: 1, H0637: 1 S0046: 1 | | | |

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| | | | | | | | | S0132: 1, H0486: 1, H0090: 1, S0112: 1, T0042: 1, H0494: 1, S0210: 1, L0770: 1, L0662: 1, L0659: 1, L0665: 1, H0682: 1, L0779: 1, H0445: 1, H0653: 1 and S0424: 1. | | | |
| 86 | HWACV74 | 1145916 | 96 | 960 - 745 | 996 | | | AR089: 2, AR061: 1 H0581: 2, H0657: 1, S0358: 1, S0046: 1, S0222: 1, H0486: 1, H0551: 1, L0761: 1, L0766: 1, L0774: 1, L0659: 1, L0666: 1, L0664: 1 and H0435: 1. | | | |
| 87 | HWAFW39 | 947915 | 97 | 188 - 370 | 997 | | Ser-26 to Ser-33. | AR089: 2, AR061: 1 H0255: 1 and H0581: 1. | | | |
| 88 | HWBBER65 | 1156447 | 98 | 2076 - 1705 | 998 | | Lys-1 to Gln-8, Gln-28 to Gly-34, Pro-46 to Arg-51. | AR089: 28, AR061: 24 L0748: 2, H0580: 1 and H0421: 1. | | | |
| 89 | HWME65 | 969190 | 99 | 2 - 382 | 999 | | Asp-30 to Trp-35, Ser-38 to Arg-43. | AR089: 17, AR061: 11 S0358: 2 and H0539: 1. | | | |
| 90 | HISBG28 | 920850 | 100 | 184 - 816 | 1000 | | Leu-91 to Glu-98, Ile-110 to Tyr-116, Ser-160 to Thr-168, Gly-175 to His-182. | AR061: 0, AR089: 0 L0766: 10, L0779: 3, L0759: 2, S0114: 1, S0116: 1, H0431: 1, | | | |

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| 91 | HAAJAB60 | 786337 | 101 | 3 - 377 | 1001 | Pro-32 to His-49. | H0013: 1, H0251: 1, H0628: 1, H0646: 1, L0761: 1, L0662: 1, L0776: 1, L0665: 1, H0702: 1, H0520: 1, H0539: 1, L0749: 1, L0750: 1, H0444: 1, H0445: 1 and H0543: 1. AR089: 1, AR061: 1 L0439: 13, L0740: 12, q13.31 H0046: 10, H0556: 9, L0752: 9, H0052: 7, H0617: 7, L0748: 7, L0758: 7, S0222: 6, L0754: 6, S0049: 5, H0620: 5, S0002: 5, L0769: 5, L0438: 5, L0741: 5, L0731: 5, S0278: 4, H0599: 4, S0010: 4, L0163: 4, L0804: 4, L0663: 4, H0144: 4, H0521: 4, L0742: 4, L0743: 4, L0751: 4, L0753: 4, H0657: 3, H0618: 3, H0050: 3, L0471: 3, S0051: 3, T0010: 3, S6028: 3, H0266: 3, H0551: 3, H0494: 3, S0144: 3, H0529: 3, | 22q13.2- q13.31 | 188826, 250100, 250800, 250800 | |
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| L0763: 3, L0770: 3, L0771: 3, L0766: 3, L0775: 3, L0659: 3, L0809: 3, L0666: 3, S0330: 3, H0696: 3, L0747: 3, L0757: 3, L0759: 3, H0265: 2, H0656: 2, S0418: 2, L0149: 2, H0333: 2, H0427: 2, H0042: 2, H0590: 2, H0457: 2, H0041: 2, S0003: 2, T0006: 2, S0364: 2, H0124: 2, S0366: 2, H0135: 2, L0638: 2, L0637: 2, L0372: 2, L0662: 2, L0776: 2, L0655: 2, L0789: 2, S0374: 2, H0658: 2, H0660: 2, S0152: 2, L0485: 2, L0599: 2, L0601: 2, H0506: 2, S0040: 1, H0650: 1, H0341: 1, S0212: 1, S0282: 1, H0663: 1, H0459: 1, H0638: 1, S0420: 1, L0617: 1, S0360: 1, S0408: 1, H0208: 1, S0132: 1, H0645: 1, H0370: 1, L0622: 1, L0623: 1, |
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| | | | | | | | | | L0783: 1, L0529: 1, L0787: 1, L0665: 1, H0519: 1, S0380: 1, H0522: 1, H0436: 1, H0576: 1, L0609: 1, L0744: 1, L0745: 1, L0749: 1, L0786: 1, L0777: 1, L0755: 1, H0444: 1, L0584: 1, L0595: 1, S0011: 1, H0422: 1 and H0008: 1. | | | | |
| 92 | HDPDE32 | 1217181 | 102 | 39 - 890 | 1002 | Arg-25 to Glu-30. | | | AR089: 10, AR061: 3 H0703: 7, H0494: 3, H0699: 3, H0542: 3, H0546: 1, H0684: 1, H0521: 1, S0031: 1 and H0543: 1. | | | | |
| 93 | HBDAC79 | 973342 1199232 | 700 103 | 165 - 647 82 - 477 | 1600 1003 | Asn-1 to Arg-6. Lys-12 to Lys-19, Phe-48 to Phe-57, Gly-120 to Gly-126. | | | AR089: 2, AR061: 1 H0556: 2, L0766: 2, S0418: 1, S0442: 1, H0393: 1, H0261: 1, S0222: 1, H0545: 1, H0050: 1, S6028: 1, H0551: 1, H0494: 1, S0144: 1, S0002: 1, H0529: 1, H0521: 1, L0439: 1, L0759: 1, S0308: 1, L0366: 1 and H0506: 1. | | | | |

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| 94 | HEMDX48 | 935414 | 701 | 1 - 366 | 1601 | Met-4 to Lys-12, Phe-41 to Phe-50. Ala-32 to Thr-39, Glu-88 to Lys-107, Thr-165 to Tyr-172, Thr-204 to Lys-210, Thr-262 to Gly-271, Thr-335 to Leu-343, Arg-476 to Leu-482, Ser-504 to Cys-514, Gln-592 to Val-608, Pro-623 to Cys-628. | AR061: 7, AR089: 3 L0666: 4, L0747: 4, L0783: 3, L0665: 3, L0602: 3, S0222: 2, H0318: 2, H0553: 2, H0135: 2, L0763: 2, L0772: 2, L0662: 2, H0660: 2, H0436: 2, L0743: 2, L0751: 2, L0750: 2, L0411: 1, H0265: 1, H0556: 1, H0685: 1, S0418: 1, S0420: 1, S0358: 1, S0046: 1, L0717: 1, H0351: 1, S6014: 1, H0431: 1, H0486: 1, H0013: 1, H0253: 1, H0052: 1, L0157: 1, H0271: 1, H0617: 1, H0090: 1, H0494: 1, H0396: 1, H0509: 1, H0652: 1, S0002: 1, S0426: 1, L0769: 1, L0764: 1, L0767: 1, L0766: 1, L0775: 1, L0806: 1, L0809: 1, T0068: 1, H0693: 1, L0352: 1, H0520: 1, |
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| | | | | | | | H0547: 1, S0152: 1, H0521: 1, S0404: 1, H0555: 1, S0027: 1, S0028: 1, L0779: 1, L0780: 1, L0752: 1, L0755: 1, L0731: 1, L0758: 1, H0707: 1, L0593: 1, L0603: 1, H0136: 1 and S0242: 1. | | |
| 95 | HHASB48 | 521844 | 702 | 1 - 321 | 1602 | Thr-47 to Gly-56. | | | |
| | | 721150 | 105 | 46 - 651 | 1005 | Ala-32 to Thr-39, Glu-88 to Lys-107, Thr-165 to Tyr-172. | AR061: 0, AR089: 0 L0666: 4, L0747: 4, L0783: 3, L0665: 3, L0602: 3, S0222: 2, H0318: 2, H0553: 2, H0135: 2, L0763: 2, L0772: 2, L0662: 2, H0660: 2, H0436: 2, L0743: 2, L0751: 2, L0750: 2, L0411: 1, H0265: 1, H0556: 1, H0685: 1, S0418: 1, S0420: 1, S0358: 1, S0046: 1, L0717: 1, H0351: 1, S6014: 1, H0431: 1, H0486: 1, H0013: 1, H0253: 1, H0052: 1, L0157: 1, H0271: 1, H0617: 1, H0090: 1, H0494: 1 | | |

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| 96 | HLWCA17 | 1104762 | 106 | 326 - 1012 | 1006 | | | | H0396: 1, H0509: 1, H0652: 1, S0002: 1, S0426: 1, L0769: 1, L0764: 1, L0767: 1, L0766: 1, L0775: 1, L0806: 1, L0809: 1, T0068: 1, H0693: 1, L0352: 1, H0520: 1, H0547: 1, S0152: 1, H0521: 1, S0404: 1, H0555: 1, S0027: 1, S0028: 1, L0779: 1, L0780: 1, L0752: 1, L0755: 1, L0731: 1, L0758: 1, H0707: 1, L0593: 1, L0603: 1, H0136: 1 and S0242: 1. | | | |
| | | | | | | | | | AR089: 13, AR061: 4 S0358: 1, S0046: 1, H0592: 1, H0036: 1, H0318: 1, S0003: 1, H0553: 1, L0766: 1, H0672: 1, L0439: 1, L0756: 1, L0755: 1, L0731: 1 and L0757: 1. | | | |
| 97 | HNTTD09 | 1104487 | 107 | 152 - 940 | 1007 | | | | AR061: 1, AR089: 0 H0656: 1, H0587: 1, H0036: 1, H0590: 1, L0143: 1, H0547: 1 | | | |

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| 98 | HSKDT07 | 676665 | 704 | 3 - 425 | 1604 | AR061: 7, AR089: 4 L0666: 4, L0747: 4, L0783: 3, L0665: 3, L0602: 3, S0222: 2, H0318: 2, H0553: 2, H0135: 2, L0763: 2, L0772: 2, L0662: 2, H0660: 2, H0436: 2, L0743: 2, L0751: 2, L0750: 2, L0411: 1, H0265: 1, H0556: 1, H0685: 1, S0418: 1, S0420: 1, S0358: 1, S0046: 1, L0717: 1, H0351: 1, S6014: 1, H0431: 1, H0486: 1, H0013: 1, H0253: 1, H0052: 1, L0157: 1, H0271: 1, H0617: 1, H0090: 1, H0494: 1, H0396: 1, H0509: 1, H0652: 1, S0002: 1, S0426: 1, L0769: 1, L0764: 1, L0767: 1, L0766: 1, L0775: 1, L0806: 1, L0809: 1, T0068: 1, H0693: 1, L0352: 1, H0520: 1 | H0689: 1 and H0653: 1. | | |
| | | 927823 | 108 | 1 - 918 | 1008 | | | | |

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| | | | | | | | | | H0547: 1, S0152: 1, H0521: 1, S0404: 1, H0555: 1, S0027: 1, S0028: 1, L0779: 1, L0780: 1, L0752: 1, L0755: 1, L0731: 1, L0758: 1, H0707: 1, L0593: 1, L0603: 1, H0136: 1 and S0242: 1. | | |
| 99 | HSRDB26 | 1102231 | 109 | 21 - 410 | 1009 | | | | AR089: 1, AR061: 1 S0022: 1, S0028: 1 and S0260: 1. | | |
| 100 | HAPBS07 | 525475 967325 | 705 110 | 15 - 347 1 - 315 | 1605 1010 | | | Glu-44 to Pro-49. | AR061: 5, AR089: 2 S0002: 4, S0344: 3, S0278: 2, S0358: 1, H0042: 1, H0575: 1, S0010: 1, H0373: 1, S0003: 1, H0163: 1, H0038: 1, H0616: 1, H0264: 1, H0100: 1, S0144: 1 and H0521: 1. | | |
| 101 | HAUAI17 | 921674 | 111 | 118 - 780 | 1011 | | | Lys-50 to Gly-55, Thr-73 to Val-78, Thr-85 to Arg-91, Pro-103 to Ser-112, Leu-199 to Ser-207, Pro-209 to Ser-214. | AR061: 2, AR089: 1 L0803: 6, L0748: 5, L0749: 4, H0424: 3, L0804: 3, L0774: 3, L0779: 3, H0213: 2, S0142: 2, L0789: 2, L0745: 2, L0731: 2, H0294: 1, H0254: 1, | | |

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| 102 | HBCBT19 | 959953 | 112 | 136 - 585 | 1012 | Asp-40 to Arg-48, Ser-68 to Ile-73, Asn-79 to His-84. | AR061: 7, AR089: 4 L0803: 6, L0766: 3, L0758: 3, L0790: 2, L0743: 2, L0748: 2, L0747: 2, L0750: 2, L0779: 2, L0755: 2, H0255: 1, H0370: 1, H0530: 1, H0150: 1, S0344: 1, L0763: 1, L0769: 1, L0637: 1, L0764: 1, L0804: 1, L0774: 1, L0805: 1, L0776: 1, L0783: 1, L0809: 1, L0664: 1, L0665: 1, L0752: 1, L0731: 1, L0681: 1 and H0543: 1. | H0393: 1, H0549: 1, H0427: 1, H0156: 1, T0082: 1, H0052: 1, H0150: 1, H0024: 1, H0135: 1, H0268: 1, H0100: 1, S0344: 1, L0763: 1, L0769: 1, L0662: 1, L0775: 1, L0805: 1, L0657: 1, L0666: 1, H0144: 1, L0740: 1, L0750: 1 and L0755: 1. | | |
| 103 | HBCPT10 | 957631 | 113 | 260 - 838 | 1013 | | AR061: 2, AR089: 2 | | | |

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| 104 | HBGDA14 | 866258 | 114 | 3 - 503 | 1014 | Gln-9 to Gln-16, Thr-33 to Gly-42, Gly-94 to Gln-101, Asp-108 to Arg-114. | AR061: 794, AR089: 295 S0050: 2, S0031: 2, S0260: 2, H0181: 1, H0617: 1 and S0390: 1. | | | | | |
| 105 | HCHNJ32 | 934848 | 115 | 3 - 764 | 1015 | Thr-1 to Ser-9, Ser-146 to Thr-154, Thr-200 to Lys-208. | AR061: 113, AR089: 26 L0748: 15, L0581: 11, H0510: 9, H0617: 9, L0755: 7, H0484: 6, H0673: 6, L0769: 6, L0758: 5, S0278: 4, H0327: 4, H0124: 4, L0774: 4, L0526: 4 | | | | | |

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| 107 | HCUGN19 | 716989 | 117 | 35 - 382 | 1017 | Glu-58 to Gly-64, Pro-77 to Cys-93, Pro-96 to Pro-106. | Glu-153 to Leu-159, Gln-162 to Gly-168, Ser-198 to Gly-203, Lys-210 to Asn-215, Gly-219 to Gln-224. | L0766: 4, L0803: 4, L0749: 3, S0358: 2, H0574: 2, H0327: 2, H0539: 2, L0758: 2, S0026: 2, S0212: 1, H0484: 1, S0354: 1, S0046: 1, H0592: 1, T0114: 1, H0427: 1, H0590: 1, H0581: 1, H0046: 1, H0081: 1, H0015: 1, H0051: 1, T0006: 1, H0040: 1, H0268: 1, S0438: 1, S0422: 1, H0529: 1, L0763: 1, L0770: 1, L0662: 1, L0794: 1, L0649: 1, L0775: 1, L0515: 1, L0792: 1, H0520: 1, H0547: 1, H0435: 1, S0328: 1, S0380: 1, S0152: 1, H0521: 1, L0356: 1, L0747: 1, L0753: 1, L0485: 1 and H0423: 1. | | |
| 108 | HCUGR38 | 706471 | 118 | 3 - 317 | 1018 | Ser-2 to His-7, Pro-14 to Leu-20, Ala-33 to Gly-38 | Glu-58 to Gly-64, Pro-77 to Cys-93, Pro-96 to Pro-106. | AR089: 7, AR061: 2 L0744: 3, L0766: 2, H0402: 1 and L0754: 1. | | |

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| 109 | HDPND85 | 852628 | 119 | 68 - 853 | 1019 | Ser-1 to Pro-10. | AR089: 0, AR061: 0 L0747: 6, H0638: 3, L0758: 3, L0157: 2, H0529: 2, L0764: 2, L0774: 2, L0776: 2, H0521: 2, H0522: 2, L0779: 2, L0603: 2, H0662: 1, S0358: 1, S0222: 1, H0038: 1, H0625: 1, S0448: 1, L0371: 1, L0770: 1, L0796: 1, L0775: 1, L0809: 1, L0791: 1, L0666: 1, H0144: 1, H0520: 1, H0436: 1, L0748: 1, L0755: 1 and L0731: 1. | | |
| 110 | HDPN38 | 883658 | 120 | 78 - 749 | 1020 | Leu-60 to Gln-65, Arg-76 to Val-81. | AR089: 11, AR061: 3 H0510: 2, L0666: 2, L0740: 2, L0595: 2, H0657: 1, H0580: 1, H0619: 1, H0357: 1, H0632: 1, H0013: 1, H0024: 1, H0578: 1, H0591: 1, H0509: 1, L0769: 1, L0804: 1, L0774: 1, L0805: 1, L0776: 1, L0527: 1, H0521: 1, H0555: 1, L0749: 1, L0757: 1 and | | |

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| 111 | HE8AM92 | 952610 | 121 | 157 - 603 | 1021 | Met-9 to Glu-16, Glu-41 to Trp-47, Arg-55 to Glu-62, Asp-135 to Pro-149. | H0423: 1, AR061: 28, AR089: 11 L0439: 21, L0438: 13, H0144: 6, H0521: 6, H0543: 5, H0013: 4, S0003: 4, L0740: 4, L0766: 3, L0759: 3, L0588: 3, S0116: 2, H0662: 2, S0358: 2, L0738: 2, H0046: 2, S0214: 2, H0039: 2, H0591: 2, H0264: 2, H0560: 2, L0770: 2, L0764: 2, L0803: 2, L0774: 2, L0659: 2, L0666: 2, H0670: 2, H0672: 2, L0743: 2, L0749: 2, L0752: 2, L0731: 2, L0758: 2, H0445: 2, H0170: 1, H0265: 1, H0583: 1, H0657: 1, S0282: 1, S0376: 1, S0360: 1, H0580: 1, H0261: 1, S0222: 1, H0586: 1, H0497: 1, L0021: 1, H0575: 1, H0036: 1, H0318: 1, H0581: 1, H0251: 1, T0115: 1, L0040: 1, H0327: 1, | | |
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| | | | | | | | S0388: 1, T0010: 1, H0266: 1, H0687: 1, S0250: 1, S0022: 1, H0622: 1, S0036: 1, H0090: 1, H0040: 1, T0067: 1, H0488: 1, H0413: 1, H0494: 1, S0150: 1, H0641: 1, S0002: 1, L0598: 1, H0529: 1, L0374: 1, L0771: 1, L0773: 1, L0521: 1, L0794: 1, L0775: 1, L0655: 1, L0606: 1, L0657: 1, L0663: 1, S0374: 1, H0520: 1, S0126: 1, H0659: 1, S0152: 1, S0432: 1, S0028: 1, L0750: 1, L0779: 1, L0777: 1, H0707: 1, L0589: 1, L0599: 1, L0593: 1, H0136: 1, S0242: 1, H0423: 1 and H0422: 1. | | |
| 112 | HE9RE21 | 888243 | 122 | 3 - 422 | 1022 | Arg-3 to Ser-15, Ser-103 to Gln-111. | AR089: 10, AR061: 3 H0556: 1, S0114: 1, S0134: 1, S0360: 1, T0082: 1, H0052: 1, H0644: 1, H0551: 1, L0770: 1, L0789: 1. | | |

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| | | | | | | | | | H0144: 1, H0435: 1 and H0436: 1. | | | |
| 113 | HETKH30 | 884009 | 123 | 90 - 884 | 1023 | Arg-1 to Lys-8. | | | AR061: 1, AR089: 1 H0046: 5, H0040: 2, H0519: 2, L0439: 2, L0758: 2, H0575: 1 and T0042: 1. | | | |
| 114 | HHAME78 | 840939 | 124 | 3 - 263 | 1024 | | | | AR089: 1, AR061: 1 H0624: 1, S0420: 1, S0366: 1, H0135: 1, H0494: 1, S0422: 1, L0745: 1 and L0758: 1. | | | |
| 115 | HKABI68 | 856590 | 125 | 1 - 471 | 1025 | Arg-20 to Arg-30, Arg-74 to Lys-82. | | | AR089: 23, AR061: 12 S0046: 1, H0100: 1, H0494: 1, H0521: 1, H0522: 1 and S0028: 1. | | | |
| 116 | HKMLN95 | 914083 | 126 | 2 - 583 | 1026 | | | | AR089: 7, AR061: 2 S0003: 5, S0354: 2, S0214: 2, H0519: 2, H0689: 2, H0522: 2, L0748: 2, L0439: 2, L0731: 2, L0759: 2, H0171: 1, T0002: 1, S0040: 1, H0669: 1, S0356: 1, S0360: 1, H0431: 1, H0586: 1, H0574: 1, H0632: 1, H0156: 1, H0590: 1, T0110: 1, L0471: 1, S6028: 1, H0628: 1, | | | |

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| | | | | | | | | | S0036: 1, H0494: 1, S0450: 1, S0144: 1, L0803: 1, L0438: 1, H0520: 1, H0547: 1, H0660: 1, S0328: 1, H0521: 1, S0434: 1, L0605: 1, L0599: 1, L0593: 1 and H0543: 1. | | | |
| 117 | HMCFA91 | 959954 | 127 | 1 - 729 | 1027 | Cys-1 to Ala-10. | | | AR061: 87, AR089: 61 L0803: 6, L0766: 3, L0758: 3, L0790: 2, L0743: 2, L0748: 2, L0747: 2, L0750: 2, L0779: 2, L0755: 2, H0255: 1, H0370: 1, H0530: 1, H0150: 1, S0344: 1, L0763: 1, L0769: 1, L0637: 1, L0764: 1, L0804: 1, L0774: 1, L0805: 1, L0776: 1, L0783: 1, L0809: 1, L0664: 1, L0665: 1, L0752: 1, L0731: 1, L0681: 1 and H0543: 1. | | | |
| 118 | HNTBF75 | 836701 | 128 | 43 - 330 | 1028 | | | | AR089: 13, AR061: 5 S0003: 5, S0354: 2, S0214: 2, H0519: 2, H0689: 2, H0522: 2, L0748: 2, L0439: 2, | | | |

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| | | | | | | | | | L0731: 2, L0759: 2, H0171: 1, T0002: 1, S0040: 1, H0669: 1, S0356: 1, S0358: 1, S0360: 1, H0431: 1, H0586: 1, H0574: 1, H0632: 1, H0156: 1, H0575: 1, H0590: 1, T0110: 1, L0471: 1, S6028: 1, H0628: 1, S0036: 1, H0494: 1, S0450: 1, S0144: 1, L0803: 1, L0809: 1, L0438: 1, H0520: 1, H0547: 1, H0660: 1, S0328: 1, H0521: 1, S0434: 1, L0605: 1, L0599: 1, L0593: 1, H0668: 1 and H0543: 1. | | | |
| 119 | HPTGB43 | 726460 | 129 | 3 - 266 | 1029 | His-1 to Ser-8, Thr-68 to Lys-76. | | | AR089: 9, AR061: 7 | | | |
| 120 | HPTVL90 | 509487 | 130 | 2 - 211 | 1030 | Pro-48 to Ile-54. | | | AR061: 1, AR089: 0 L0803: 6, L0748: 5, L0749: 4, H0424: 3, L0804: 3, L0774: 3, L0779: 3, H0213: 2, S0142: 2, L0789: 2, L0745: 2, L0731: 2, H0294: 1, H0254: 1, H0393: 1 H0549: 1 | | | |

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| 121 | HSKIA89 | 837986 | 131 | 296 - 634 | 1031 | | | | H0427: 1, H0156: 1, T0082: 1, H0052: 1, H0150: 1, H0024: 1, H0135: 1, H0268: 1, H0100: 1, S0344: 1, L0763: 1, L0769: 1, L0662: 1, L0775: 1, L0805: 1, L0657: 1, L0666: 1, H0144: 1, L0740: 1, L0750: 1 and L0755: 1. | | |
| 122 | HTXGF27 | 695766 | 132 | 1 - 1011 | 1032 | Gly-1 to Gly-6, Ser-16 to Ala-23, Thr-114 to Lys-120, Thr-274 to Ser-280, Arg-327 to Ser-337. | | | AR089: 8, AR061: 2 L0471: 1, S0150: 1, H0435: 1, H0539: 1 and S3014: 1. AR061: 3, AR089: 3 L0769: 5, L0752: 5, S0358: 4, H0448: 4, L0754: 4, H0052: 3, L0773: 3, L0666: 3, L0740: 3, L0750: 3, L0596: 3, H0370: 2, H0024: 2, H0083: 2, H0031: 2, H0090: 2, S0142: 2, L0766: 2, L0663: 2, L0747: 2, L0753: 2, L0588: 2, L0599: 2, H0265: 1, S0040: 1, H0583: 1, H0656: 1 S0442: 1 | | |

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| 123 | HWHHW54 | 684125 | 133 | 853 - 1146 | 1033 | Pro-50 to Gly-69, Pro-71 to Lys-80. | H0393: 1, H0431: 1, L0622: 1, H0635: 1, S0280: 1, L0021: 1, H0002: 1, H0036: 1, H0421: 1, H0204: 1, H0046: 1, H0014: 1, H0015: 1, S6028: 1, H0266: 1, H0169: 1, S0366: 1, H0040: 1, H0264: 1, S0038: 1, H0494: 1, L0772: 1, L0372: 1, L0374: 1, L0644: 1, L0765: 1, L0771: 1, L0364: 1, L0806: 1, L0659: 1, L0783: 1, L0647: 1, L0665: 1, H0435: 1, H0658: 1, H0214: 1, L0751: 1, L0731: 1, L0758: 1, L0759: 1, H0653: 1, L0462: 1 and H0352: 1. | | |
| 124 | HWHPO29 | 857383 | 134 | 236 - 670 | 1034 | | AR089: 3, AR061: 1 L0748: 6, L0747: 2, H0170: 1, H0586: 1, S0051: 1, H0163: 1, L0665: 1, H0670: 1, H0660: 1 and H0423: 1. | | |

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| 125 | HWLPR94 | 967326 | 135 | 184 - 459 | 1035 | Thr-29 to Gly-34, Glu-53 to Leu-58, Thr-66 to Thr-74. | L0439: 2, H0592: 1, H0587: 1, L0021: 1, L0456: 1, H0494: 1, S0448: 1, L0662: 1 and L0774: 1. AR089: 18, AR061: 3 L0766: 4, L0666: 3, S0278: 2, L0758: 2, S0358: 1, S0376: 1, S0010: 1, H0050: 1, S0003: 1, H0038: 1, H0616: 1, H0264: 1, H0100: 1, S0448: 1, S0344: 1, S0002: 1, S0426: 1, L0642: 1, L0659: 1, S0374: 1, H0521: 1 and : 1. | | | | |
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| 126 | HWLUL28 | 925331 | 136 | 1 - 750 | 1036 | Arg-11 to Pro-19, Pro-36 to Asp-44, Lys-183 to Gly-189, Thr-201 to Arg-207. | AR089: 16, AR061: 9 L0439: 3, S0360: 2, H0615: 2, L0770: 2, L0666: 2, L0438: 2, L0749: 2, L0758: 2, L0596: 2, H0294: 1, H0351: 1, S0222: 1, H0441: 1, H0611: 1, H0599: 1, H0251: 1, H0046: 1, H0567: 1, H0081: 1, H0083: 1, H0213: 1, H0617: 1, L0055: 1, H0494: 1, H0560: 1, L0769: 1, L0761: 1, L0766: 1, L0649: 1, L0774: 1, L0775: 1, L0375: 1, L0805: 1, L0657: 1, L0526: 1, L0789: 1, L0665: 1, H0519: 1, H0658: 1, S0380: 1, L0748: 1, L0786: 1, L0777: 1, L0731: 1 and H0543: 1. | 16p13.3 | 141750, 141800, 141800, 141800, 141800, 141850, 141850, 141850, 141850, 156850, 186580, 191092, 600140, 600273, 601313, 601785 |
| 127 | HWLXT48 | 957630 | 137 | 55 - 363 | 1037 | | AR089: 12, AR061: 9 S0360: 2, H0550: 2, S0028: 2, H0543: 2, H0663: 1, H0638: 1, S0376: 1, H0580: 1, S0045: 1, H0393: 1, | | |

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| 128 | HBGMD15 | 1103922 | 138 | 1 - 567 | 1038 | Gly-1 to Ser-6. | H0370: 1, H0392: 1, H0156: 1, H0618: 1, H0318: 1, H0135: 1, T0042: 1, H0366: 1, S0002: 1, L0803: 1, L0791: 1, S0126: 1, S0037: 1, S0027: 1, S0032: 1, L0741: 1, L0754: 1, H0445: 1, L0596: 1, S0026: 1 and H0542: 1. | | |
| 129 | HNGMA91 | 786307 789744 | 706 139 | 3 - 323 7 - 327 | 1606 1039 | His-53 to Arg-61. His-8 to Gly-18. | AR089: 0, AR061: 0 H0617: 4 and S0028: 1. | | |
| 130 | HSLEI57 | 1103672 730927 | 140 707 | 2 - 640 2 - 433 | 1040 1607 | Gly-23 to Gly-28, Arg-73 to Asn-78. | AR089: 1, AR061: 0 S0044: 1 and S0028: 1. | | |
| 131 | HSLFE21 | 1103524 | 141 | 2 - 1012 | 1041 | Pro-52 to Ala-57, Tyr-110 to Lys-122. | AR061: 1, AR089: 1 H0246: 4, S0028: 3, H0197: 2, S0282: 1, H0199: 1 and S3020: 1. | | |
| 132 | HSLIE40 | 823083 1105422 | 708 142 | 122 - 658 510 - 1 | 1608 1042 | | AR061: 5, AR089: 2 H0294: 1, S0044: 1 and S0028: 1. | | |
| 133 | HTXHA35 | 866274 1152110 | 709 143 | 65 - 283 291 - 839 | 1609 1043 | His-49 to Lys-54. Gln-130 to Asp-135, | AR061: 6, AR089: 3 | | |

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| | | | | | | | | | H0124: 2, H0135: 2, H0265: 1, S0134: 1, H0657: 1, S0280: 1, H0122: 1, H0618: 1, H0251: 1, H0090: 1, H0646: 1, H0144: 1, L0743: 1 and L0748: 1. | | |
| 134 | HAICS07 | 633682 1105538 | 710 144 | 247 - 501 157 - 810 | 1610 1044 | Gly-75 to Cys-83. | Asp-167 to Leu-178. | | AR089: 6, AR061: 6 S0132: 1, H0038: 1 and L0439: 1. | | |
| | | 953351 | 711 | 157 - 810 | 1611 | Met-104 to His-110, Arg-202 to Pro-214. | | | | | |
| 135 | HBKDN33 | 1167313 | 145 | 2 - 1015 | 1045 | Ser-28 to Pro-34, Pro-134 to Ser-139, Gln-178 to Gly-183, Thr-193 to Gly-198, His-244 to Gly-257, Asp-263 to Tyr-273. | | | AR089: 1, AR061: 0 L0439: 2, H0506: 2, S0354: 1, S0358: 1, S0280: 1, H0622: 1, S0366: 1, H0059: 1, S0344: 1, H0658: 1, H0539: 1, H0521: 1, H0522: 1, H0555: 1, L0748: 1, L0751: 1, L0753: 1 and L0596: 1. | | |
| | | 922414 | 712 | 2 - 1237 | 1612 | Ser-28 to Pro-34, Pro-134 to Ser-139, Gln-178 to Gly-183, Thr-193 to Gly-198, His-244 to Gly-257, Asp-263 to Tyr-273, Lys-337 to Arg-347, | | | | | |

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| 136 | HBODH62 | 1228278 | 146 | 293 - 1729 | 1046 | Pro-366 to Lys-372, Ala-382 to Asp-387. Gln-10 to Gly-15, Lys-193 to Ser-199, Asp-323 to Tyr-332, Leu-425 to Gly-431, Lys-470 to Ala-477. | AR089: 0, AR061: 0 H0046: 5, L0769: 5, L0755: 4, L0758: 4, H0581: 3, L0803: 3, L0774: 3, L0600: 3, L0427: 2, S0358: 2, H0253: 2, H0252: 2, H0553: 2, H0087: 2, S0038: 2, L0517: 2, L0438: 2, L0748: 2, L0756: 2, L0777: 2, H0170: 1, H0265: 1, H0650: 1, H0657: 1, S0116: 1, S0442: 1, S0354: 1, H0370: 1, H0486: 1, H0013: 1, H0349: 1, H0706: 1, H0618: 1, H0327: 1, H0373: 1, H0428: 1, S0364: 1, H0124: 1, H0100: 1, L0770: 1, L0637: 1, L0761: 1, L0372: 1, L0800: 1, L0641: 1, L0768: 1, L0794: 1, L0766: 1, L0657: 1, L0635: 1, L0542: 1, L0809: 1, L0789: 1, L0666: 1, |
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| 137 | HCEPJ44 | 742827 1157810 | 713 147 | 3 - 290 2 - 571 | 1613 1047 | Gln-1 to Asp-8, Lys-142 to Asp-160. | L0665: 1, H0144: 1, H0682: 1, H0651: 1, S0380: 1, H0555: 1, L0439: 1, L0750: 1, L0780: 1, L0759: 1, L0366: 1, H0543: 1 and H0506: 1. | | |
| 138 | HCWCM65 | 930790 1105668 | 714 148 | 3 - 536 3 - 659 | 1614 1048 | Lys-130 to Asp-148. Ser-44 to His-57. | AR089: 6, AR061: 4 S0420: 1, H0052: 1, H0024: 1, H0649: 1, H0689: 1 and H0435: 1. | | |
| 139 | HDQDY52 | 529230 1182322 | 715 149 | 1 - 360 43 - 597 | 1615 1049 | Ser-45 to His-58. His-68 to Gly-73, Glu-81 to Glu-87. | AR089: 25, AR061: 24 H0521: 2, H0580: 1, H0393: 1, H0052: 1, H0081: 1, L0774: 1 and S0152: 1. | | |
| 140 | HHEAA32 | 852622 1203140 | 716 150 | 43 - 597 499 - 1236 | 1616 1050 | His-68 to Gly-73, Glu-81 to Glu-87. Arg-19 to Gln-28, Glu-35 to Ser-40, Gly-60 to Tyr-66. | AR061: 9, AR054: 6, AR089: 3, AR050: 1, AR051: 1 H0574: 2, H0510: 2, H0549: 1, H0331: 1, S0010: 1 and L0775: 1. | | |

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| 141 | HEGAN70 | 839719 | 717 | 3 - 407 | 1617 | Leu-8 to Lys-14, Asp-53 to Gly-58, Met-76 to Asp-82. Asn-1 to Thr-7. | AR089: 2, AR061: 2 H0620: 2, H0550: 1, H0529: 1, L0775: 1, S0390: 1 and H0665: 1. |
| 142 | HFKMF42 | 1104119 | 152 | 56 - 1117 | 1052 | | AR061: 12, AR089: 6 L0766: 4, H0617: 3, H0135: 3, L0769: 2, L0438: 2, H0265: 1, S0282: 1, H0662: 1, S0358: 1, S0360: 1, S0045: 1, H0431: 1, L0586: 1, H0575: 1, H0620: 1, S0048: 1, H0428: 1, S0366: 1, H0509: 1, L0763: 1, L0796: 1, L0764: 1, L0774: 1, L0805: 1, L0776: 1, L0783: 1, L0789: 1, L0664: 1, L0665: 1, L0565: 1, L0758: 1 and S0424: 1. |
| 143 | HFPHG06 | 1104964 | 153 | 111 - 449 | 1053 | Gln-31 to Pro-46. | AR089: 0, AR061: 0 S0222: 2 |
| 144 | HHEMB89 | 1227613 | 154 | 3 - 1994 | 1054 | Val-94 to Gln-99, Arg-107 to Thr-112. | AR089: 4, AR061: 1 H0046: 5, L0769: 5. |

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| | | | | | | | | L0366: 1, H0543: 1 and H0506: 1. | | |
| | | 574897 | 720 | 1 - 465 | 1620 | | | | | |
| 145 | HLDPC46 | 466567 | 155 | 2 - 595 | 1055 | Leu-1 to Glu-6, Arg-10 to Gln-19. | | AR061: 2, AR089: 1 H0574: 2, H0510: 2, H0549: 1, H0331: 1, S0010: 1 and L0775: 1. | | |
| 146 | HLDRG44 | 1106225 | 156 | 1 - 1026 | 1056 | Gln-1 to Cys-12. | | AR061: 13, AR089: 0 L0803: 10, L0774: 9, L0775: 6, L0651: 4, L0581: 4, H0510: 2, H0632: 1, H0156: 1, L0021: 1, H0015: 1, H0388: 1, H0509: 1, L0375: 1, L0790: 1, L0748: 1 and L0749: 1. | | |
| 147 | HLICR73 | 969544 | 721 | 2 - 946 | 1621 | Asp-60 to Lys-65. | | AR061: 9, AR089: 2 H0510: 3, L0393: 1, H0355: 1 and L0581: 1. | | |
| | | 1107517 | 157 | 3 - 539 | 1057 | Asp-49 to Gly-55, Pro-73 to Thr-80, Thr-98 to Phe-103. | | | | |
| | | 837030 | 722 | 1 - 444 | 1622 | Asp-41 to Gly-47, Pro-65 to Thr-72, Thr-90 to Phe-95. | | | | |
| 148 | HNHOP64 | 1103943 | 158 | 524 - 3 | 1058 | Pro-51 to Phe-58. | | AR089: 22, AR061: 7 H0483: 1, H0052: 1, H0553: 1 and S0216: 1. | | |
| | | 966754 | 723 | 365 - 889 | 1623 | | | | | |
| 149 | HSDEF56 | 1128288 | 159 | 1 - 744 | 1059 | | | AR061: 0, AR089: 0 H0171: 1, T0042: 1 and S0031: 1. | | |

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| 150 | HTENI29 | 496551 | 724 | 2 - 490 | 1624 | Pro-74 to Lys-84, Gln-107 to Trp-113. | AR061: 5, AR089: 3 L0748: 6, L0749: 6, L0758: 6, L0439: 5, L0794: 4, L0805: 3, L0438: 3, S0116: 2, H0574: 1, N0006: 1, H0616: 1, L0515: 1, L0809: 1, L0756: 1 and L0753: 1. | | |
| 151 | HWMKD72 | 954519 1106729 | 725 161 | 3 - 1172 2 - 652 | 1625 1061 | Asp-1 to Arg-7. Thr-95 to Gly-106, Pro-188 to Ser-193. | AR089: 2, AR061: 1 L0803: 12, S0358: 2, L0748: 2, H0643: 1, H0494: 1, L0065: 1, L0800: 1, L0774: 1, L0657: 1, S0152: 1 and L0755: 1. | | |
| 152 | HAPSQ21 | 970613 972037 | 726 162 | 2 - 652 1 - 864 | 1626 1062 | Thr-95 to Gly-106, Pro-188 to Ser-193. Gly-48 to Glu-54, Pro-107 to His-112, His-122 to Ala-128, Arg-225 to Gly-232. | AR061: 2, AR089: 2 H0575: 6, H0042: 2, H0024: 2, L0774: 2, L0750: 2, L0599: 2, H0549: 1, H0375: 1, H0647: 1, H0646: 1, L0806: 1, L0791: 1 and L0779: 1. | | |
| 153 | HLJDW02 | 1192885 | 163 | 617 - 3 | 1063 | Arg-57 to Gln-76, | AR061: 2, AR089: 1 | | |

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|-----|---------|--------|---------|-----|---------|------|------|---|---|--|--|
| 154 | HMGBT01 | 837592 | 1205666 | 727 | 2 - 517 | 1627 | 1064 | <p>Glu-86 to Cys-98, Pro-112 to Cys-122, Ser-132 to Gly-143.</p> <p>Asp-1 to Gln-9, Leu-45 to Lys-62, Thr-69 to Glu-74, Pro-189 to Trp-194, Ile-205 to Leu-210, Tyr-217 to Ser-222, Ser-249 to Asp-256, Thr-311 to Tyr-317, Arg-344 to Ile-349.</p> | <p>H0549: 1, H0575: 1, H0375: 1, H0647: 1, L0774: 1 and L0779: 1.</p> <p>AR050: 12, AR054: 10, AR051: 2, AR089: 2, AR061: 0 L0439: 23, L0748: 18, L0438: 17, L0749: 10, L0794: 7, L0805: 6, L0740: 6, L0777: 6, H0013: 5, H0052: 5, L0770: 5, L0731: 5, L0803: 4, L0754: 4, L0750: 4, L0779: 4, L0752: 4, S0040: 3, H0551: 3, H0494: 3, H0538: 3, L0776: 3, L0809: 3, S0126: 3, S0378: 3, L0742: 3, L0747: 3, L0755: 3, S0222: 2, S0010: 2, H0327: 2, H0545: 2, H0266: 2, L0351: 2, L0800: 2, L0768: 2, L0774: 2, L0806: 2, L0665: 2, S0028: 2, L0744: 2, L0745: 2, L0756: 2, L0753: 2, L0757: 2, L0758: 2,</p> | | |
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| | L0759: 2, S0031: 2, S0260: 2, L0592: 2, H0171: 1, S6024: 1, H0650: 1, H0381: 1, S0001: 1, H0580: 1, H0393: 1, S0300: 1, S6016: 1, H0333: 1, H0270: 1, H0156: 1, H0599: 1, H0251: 1, H0050: 1, L0471: 1, H0620: 1, H0051: 1, H0267: 1, H0284: 1, H0628: 1, S0036: 1, H0135: 1, H0591: 1, H0264: 1, H0268: 1, H0412: 1, S0038: 1, S0112: 1, S0002: 1, L0598: 1, L0520: 1, L0764: 1, L0767: 1, L0804: 1, L0775: 1, L0651: 1, L0515: 1, L0783: 1, L0787: 1, L0788: 1, L0790: 1, H0693: 1, L0352: 1, H0648: 1, H0521: 1, H0696: 1, S0027: 1, L0741: 1, L0743: 1, L0751: 1, L0780: 1, H0445: 1, L0596: 1, L0581: 1, H0653: 1, S0192: 1, H0506: 1 and | |
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| 155 | HSSJJ24 | 879904 1178041 | 728 165 | 3 - 395 2 - 1171 | 1628 1065 | Leu-6 to Gln-12, Leu-48 to Lys-65, Thr-72 to Glu-77, Pro-192 to Trp-197, Ile-208 to Leu-213, Tyr-220 to Ser-225, Ser-252 to Asp-259, Thr-314 to Tyr-320, Arg-347 to Ile-352. | AR061: 4, AR089: 0 L0439: 23, L0748: 18, L0438: 17, L0749: 10, L0794: 7, L0805: 6, L0740: 6, L0777: 6, H0013: 5, H0052: 5, L0770: 5, L0731: 5, L0803: 4, L0754: 4, L0750: 4, L0779: 4, L0752: 4, S0040: 3, H0551: 3, H0494: 3, H0538: 3, L0776: 3, L0809: 3, S0126: 3, S0378: 3, L0742: 3, L0747: 3, L0755: 3, S0222: 2, S0010: 2, H0327: 2, H0545: 2, H0266: 2, L0351: 2, L0800: 2, L0768: 2, L0774: 2, L0806: 2, L0665: 2, S0028: 2, L0744: 2, L0745: 2, L0756: 2, L0753: 2, L0757: 2, L0758: 2, L0759: 2, S0031: 2, S0260: 2, L0592: 2, H0171: 1, S6024: 1, H0650: 1 H0381: 1 | H0352: 1. | |
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| 157 | HNTMD81 | 929511 | 167 | 1 - 492 | 1067 | Ala-8 to Gly-14, His-44 to Ser-50, Tyr-70 to Thr-75, Ser-98 to Pro-113, Arg-119 to Phe-124, Ser-137 to Glu-154. | AR089: 5, AR061: 3 L0809: 1 and H0520: 1. | L0777: 2, H0123: 1 and L0747: 1. | 302350, 306400, 309470, 309585, 311250, 312040, 312610, 314850 |
| | | | | | | | | | 104770, 107670, 110700, 135940, 145001, 146790, 152445, 152445, 159001, 174000, 179755, 182860, 182860, 182860, 191315, 230800, 230800, 266200, 600897, 601105, 601412, 601652. |

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| 158 | HBSAJ60 | 1174334 | 168 | 2 - 1075 | 1068 | Gly-24 to Lys-36. | AR089: 1, AR061: 1 S0028: 5, S0050: 3, L0591: 3, H0381: 2, H0623: 2, S0031: 2, S6024: 1, H0255: 1, H0305: 1, S0045: 1, S0278: 1, H0013: 1, S0280: 1, L0105: 1, H0271: 1, H0687: 1, H0634: 1, S0142: 1, S0126: 1, S0152: 1 and S0027: 1. | | 602491 |
| 159 | HSKCI43 | 573965 506599 | 730 169 | 2 - 265 1 - 348 | 1630 1069 | Ala-6 to Tyr-11, Gly-21 to Lys-33, Pro-54 to Trp-61, Ala-69 to Ile-75. | AR089: 2, AR061: 1 S0028: 5, S0050: 3, L0591: 3, H0381: 2, H0623: 2, S0031: 2, S6024: 1, H0255: 1, H0305: 1, S0045: 1, S0278: 1, H0013: 1, S0280: 1, L0105: 1, H0271: 1, H0687: 1, H0634: 1, S0142: 1, S0126: 1, S0152: 1 and S0027: 1. | | |
| 160 | HSDKE47 | 1128095 764970 | 170 731 | 353 - 3 1 - 297 | 1070 1631 | Asn-42 to Gly-47, Lys-55 to Ala-62. | AR089: 15, AR061: 6 S0260: 1 and L0581: 1. | | |

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| 161 | HCWTB56 | 1172460 | 171 | 400 - 2 | 1071 | Leu-4 to Pro-10, Ser-15 to Ser-20. | AR061: 5, AR089: 4 H0305: 2 and H0589: 1. | | |
| | | 853009 | 732 | 2 - 346 | 1632 | | | | |
| 162 | HFPBS73 | 1144027 | 172 | 370 - 1149 | 1072 | Ala-72 to Asn-79, Asp-206 to Gly-211. | AR061: 7, AR089: 2 S0045: 2, S0028: 2, S0046: 1, S0222: 1, L0477: 1, H0042: 1, S3012: 1 and S0031: 1. | | |
| | | 954892 | 733 | 3 - 590 | 1633 | Ala-64 to Asn-71. | | | |
| 163 | HOEDD44 | 954893 | 173 | 44 - 583 | 1073 | | AR061: 1, AR089: 1 H0254: 2, H0255: 1, H0617: 1 and S0126: 1. | | |
| 164 | HSUAN33 | 956315 | 174 | 1617 - 190 | 1074 | Pro-28 to Lys-33, Pro-111 to Gln-116, Phe-161 to Ser-167, Pro-289 to Phe-301, Ser-305 to Asp-314. | AR061: 982, AR089: 580 L0527: 2, H0208: 1, H0635: 1, S0250: 1, H0622: 1, H0551: 1, L0766: 1, H0519: 1, H0521: 1, S0027: 1 and H0136: 1. | | |
| 165 | HBCMD49 | 1206021 | 175 | 1 - 366 | 1075 | Glu-47 to Thr-52. | AR061: 1, AR089: 0 L0774: 3, H0068: 2, L0622: 1, H0119: 1, H0509: 1, L0775: 1, L0776: 1, L0666: 1, S0028: 1, L0758: 1, S0260: 1 and S0396: 1. | | |
| | | 865314 | 734 | 2 - 619 | 1634 | Arg-1 to Leu-6, Pro-47 to Arg-52. | | | |

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| 166 | HKABN12 | 956826 | 176 | 900 - 478 | 1076 | | AR089: 12, AR061: 6 | | |
| 167 | HMOAC31 | 1228291 | 177 | 1156 - 2640 | 1077 | His-40 to Asn-46, Ser-101 to Lys-107, Ile-179 to Arg-184, Trp-223 to Cys-230, Phe-300 to Phe-306, Lys-353 to Gly-360, Leu-477 to Arg-490. | AR089: 1, AR061: 1 H0624: 2, S0001: 2, L0005: 1, S0045: 1, H0619: 1, H0191: 1, L0105: 1, H0165: 1, S0144: 1, S0428: 1 and S0031: 1. | | |
| | | 920386 | 735 | 2 - 523 | 1635 | | | | |
| 168 | HMVBQ92 | 1204710 | 178 | 1686 - 2108 | 1078 | Gly-21 to Pro-27, Gln-62 to Asp-67, Asn-117 to Leu-124, Arg-131 to Phe-138. | AR089: 22, AR061: 9 L0748: 13, H0457: 9, L0751: 7, L0665: 6, L0766: 5, L0758: 5, S0358: 4, L0774: 4, H0144: 4, L0749: 4, L0777: 4, H0014: 3, L0662: 3, L0775: 3, L0776: 3, L0743: 3, L0747: 3, L0581: 3, L0600: 3, H0052: 2, L0640: 2, L0659: 2, L0526: 2, L0809: 2, S0126: 2, H0696: 2, L0439: 2, L0746: 2, L0750: 2, L0753: 2, H0295: 1, S0134: 1, S0212: 1, S0376: 1, S0045: 1, H0619: 1, H0261: 1, H0550: 1, | | |

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| 169 | HOELA62 | 791284 | 736 | 2 - 295 | 1636 | Gly-21 to Pro-27, Gln-62 to Asp-67, Asn-117 to Leu-124. | AR061: 7, AR089: 5 L0748: 13, H0457: 9, L0751: 7, L0665: 6, L0766: 5, L0758: 5, S0358: 4, L0774: 4, H0144: 4, L0749: 4, L0777: 4, H0014: 3, L0662: 3, L0775: 3, L0776: 3, L0743: 3. | H0333: 1, H0331: 1, H0486: 1, H0427: 1, H0575: 1, H0085: 1, H0204: 1, H0046: 1, H0012: 1, H0057: 1, S0051: 1, H0510: 1, H0188: 1, H0687: 1, H0169: 1, H0090: 1, H0591: 1, T0067: 1, H0488: 1, L0374: 1, L0648: 1, L0551: 1, L0376: 1, L0807: 1, L0790: 1, L0791: 1, L0666: 1, H0547: 1, H0519: 1, H0660: 1, H0672: 1, H0539: 1, H0555: 1, H0436: 1, S0028: 1, L0752: 1, L0755: 1, L0759: 1 and S0192: 1. | | |
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| | L0747: 3, L0581: 3, L0600: 3, H0052: 2, L0640: 2, L0659: 2, L0526: 2, L0809: 2, S0126: 2, H0696: 2, L0439: 2, L0746: 2, L0750: 2, L0753: 2, H0295: 1, S0134: 1, S0212: 1, S0376: 1, S0045: 1, H0619: 1, H0261: 1, H0550: 1, H0333: 1, H0331: 1, H0486: 1, H0427: 1, H0575: 1, H0085: 1, H0204: 1, H0046: 1, H0012: 1, H0057: 1, S0051: 1, H0510: 1, H0188: 1, H0687: 1, H0169: 1, H0090: 1, H0591: 1, T0067: 1, H0488: 1, L0374: 1, L0648: 1, L0551: 1, L0376: 1, L0807: 1, L0790: 1, L0791: 1, L0666: 1, H0547: 1, H0519: 1, H0660: 1, H0672: 1, H0539: 1, H0555: 1, H0436: 1, S0028: 1, L0752: 1, L0755: 1, L0759: 1 and S0192: 1. |
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| 170 | HSSGE35 | 863712 | 737 | 1440 - 1943 | 1637 | Ser-1 to Arg-13, Glu-32 to Ser-39. | AR089: 15, AR061: 13 T0006: 1 and H0135: 1. | | | |
| | | 1228152 | 180 | 1 - 516 | 1080 | His-5 to Thr-13, Leu-26 to Ser-33, Gln-93 to Asp-98, Asn-148 to Leu-155, Arg-162 to Phe-169. | | | | |
| | | 967832 | 738 | 1 - 396 | 1638 | Ser-3 to Ser-11. | | | | |
| 171 | HEMFJ74 | 1216651 | 181 | 52 - 1368 | 1081 | Glu-11 to Ala-41, Pro-59 to Glu-64, Gly-90 to Arg-98, Glu-115 to Ser-121, Ser-150 to Gly-158, Phe-186 to Thr-192, Asp-204 to Glu-209, Ser-256 to Ser-261, Thr-283 to Asp-289, Val-341 to Ala-352, Asp-405 to Trp-422. | AR089: 16, AR061: 2 H0519: 2, S0040: 1, S0046: 1, H0455: 1, H0427: 1, H0599: 1, H0052: 1, H0038: 1, H0551: 1, H0269: 1, S0126: 1, H0689: 1, H0539: 1 and L0750: 1. | | | |
| | | 523350 | 739 | 1 - 348 | 1639 | Gly-1 to Cys-39. | | | | |
| 172 | HISCL24 | 676997 | 182 | 3 - 452 | 1082 | Phe-10 to Thr-16, Asp-28 to Glu-33. | AR089: 0, AR061: 0 H0519: 2, S0040: 1, S0046: 1, H0455: 1, H0427: 1, H0599: 1, H0052: 1, H0038: 1, H0551: 1, H0269: 1, S0126: 1, H0689: 1, H0539: 1 and L0750: 1. | 5q34-q35 | 109690, 109690, 123101, 164040, 180071, 208100, 246530, 600584 | |
| 173 | H7PBB83 | 1228150 | 183 | 1 - 1110 | 1083 | | AR061: 1, AR089: 0 S0252: 5, S0268: 5, | | | |

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| | | | | | | | | | S0256: 4, S0228: 3, S0270: 3, S0258: 2, H0305: 2, L0717: 2, H0090: 2, H0521: 2, L0740: 2, L0777: 2, H0445: 2, H0657: 1, S0212: 1, H0580: 1, H0438: 1, H0486: 1, T0074: 1, H0581: 1, S0388: 1, H0266: 1, H0412: 1, L0637: 1, L0766: 1, S0053: 1, S0380: 1, L0755: 1, L0605: 1, L0592: 1, L0581: 1, L0593: 1, H0543: 1 and H0423: 1. | | |
| | | 908235 | 740 | 756 - 301 | 1640 | Glu-87 to Thr-94. | | | AR061: 4, AR089: 2 L0742: 3, S0010: 2, H0650: 1, S6026: 1, H0068: 1, L0794: 1 and L0809: 1. | | |
| 174 | HAGBA63 | 1122199 | 184 | 1121 - 66 | 1084 | Ser-13 to Leu-22, Phe-40 to Lys-45. | | | | | |
| | | 509775 | 741 | 2 - 361 | 1641 | Ser-13 to Leu-22, Phe-40 to Lys-45. | | | | | |
| 175 | HBMUG47 | 1102698 | 185 | 3 - 551 | 1085 | Arg-1 to Lys-9. | | | AR089: 11, AR061: 11 L0665: 3, S0116: 1 and H0597: 1. | | |
| | | 863846 | 742 | 1 - 315 | 1642 | Gln-59 to Ser-71. | | | | | |
| 176 | HCRPZ84 | 1130816 | 186 | 3 - 1676 | 1086 | Ser-8 to Gln-14, Asn-52 to Pro-63. | | | AR061: 2, AR089: 1 H0662: 2, S0003: 2. | | |

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| 177 | HCWTR54 | 1192287 | 187 | 39 - 311 | 1087 | Lys-172 to Lys-183, Thr-204 to Glu-210, Thr-227 to Ile-239, Ala-251 to Lys-258, Pro-276 to Glu-286, Glu-293 to Glu-304, Asn-338 to Lys-343, Asp-350 to Lys-372, Leu-374 to Asp-380, Leu-397 to Arg-412, Tyr-419 to Ala-426, Ser-467 to Lys-479. | S0152: 2, L0356: 2, S0356: 1, S0354: 1, S0360: 1, H0013: 1, H0581: 1, H0090: 1, H0641: 1, H0435: 1, H0648: 1, H0518: 1, H0479: 1, L0731: 1, S0031: 1 and H0542: 1. | | |
| | | 965476 | 743 | 2 - 1252 | 1643 | Lys-31 to Lys-42, Thr-63 to Glu-69, Thr-86 to Ile-98, Ala-110 to Lys-117, Pro-135 to Glu-145, Glu-152 to Glu-163, Asn-197 to Lys-202, Asp-209 to Lys-231, Leu-233 to Asp-239, Leu-256 to Arg-271, Tyr-278 to Ala-285, Ser-326 to Lys-338. | | | |
| | | 729290 | 744 | 49 - 240 | 1644 | Ser-37 to Gly-44, Ile-46 to Glu-60. | AR089: 6, AR061: 2 H0589: 2 | | |
| 178 | HDPBB41 | 1195686 | 188 | 2480 - 564 | 1088 | Pro-6 to Cys-12, Val-15 to Gly-28, Arg-45 to Pro-53 | AR089: 18, AR061: 6 L0803: 5, H0640: 2, H0373: 2, H0040: 2 | | |

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| | H0412: 2, S0422: 2, L0794: 2, L0804: 2, L0655: 2, H0547: 2, L0748: 2, L0777: 2, L0759: 2, H0543: 2, H0624: 1, S0116: 1, H0341: 1, S0418: 1, S0356: 1, S0358: 1, S0360: 1, H0329: 1, L0717: 1, T0039: 1, H0013: 1, H0427: 1, H0156: 1, L0021: 1, S0182: 1, H0263: 1, H0039: 1, T0086: 1, H0628: 1, H0591: 1, H0487: 1, H0102: 1, T0041: 1, T0042: 1, H0494: 1, S0142: 1, S0002: 1, L0662: 1, L0364: 1, L0774: 1, L0805: 1, L0809: 1, L0663: 1, H0144: 1, H0702: 1, H0519: 1, H0682: 1, H0684: 1, H0659: 1, H0660: 1, H0521: 1, H0696: 1, H0555: 1, L0751: 1, L0749: 1, L0758: 1, L0593: 1, H0668: 1 and H0667: 1. | | | | | | |
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| 179 | HEOPI32 | 925800 | 745 | 2 - 667 | 1645 | Asp-37 to Ile-44, Asp-47 to Thr-52, Pro-80 to Asp-85, Ala-90 to Tyr-101, Asp-138 to Glu-146, Ser-154 to Phe-161, Asn-172 to Gln-178, Gln-185 to Glu-190, Asn-205 to Ser-215. | AR089: 1, AR061: 1 H0457: 5, L0766: 3, L0791: 2, S0420: 1, S0250: 1, L0638: 1, L0803: 1, L0806: 1, H0144: 1, H0547: 1, L0779: 1, L0485: 1 and H0423: 1. | |
| 180 | HFSAG03 | 1151479 | 190 | 716 - 360 | 1090 | Phe-8 to Asp-18, Pro-71 to Arg-84, Arg-90 to Asp-97, Ser-125 to Leu-133, Ala-137 to Gln-144, Met-181 to Gly-190, Gln-193 to Ile-199. | AR089: 18, AR061: 11 H0057: 1, L0520: 1 and L0389: 1. | |
| 181 | HFXC124 | 1182719 | 191 | 3 - 680 | 1091 | Glu-33 to Thr-45, Arg-50 to Ser-59. | AR061: 4, AR089: 2 H0361: 3, S0001: 1, S0045: 1, S0278: 1, S0144: 1 and S0053: 1. | |
| | | 908374 | 747 | 1 - 663 | 1647 | Val-2 to Val-12, Asp-20 to Glu-26, Gln-56 to Gly-61, Gly-69 to Arg-76. | | |

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| 182 | HF ^X HJ89 | 907938 | 192 | 162 - 881 | 1092 | Gly-167 to Lys-175, Pro-178 to Gly-205. | AR061: 4, AR089: 2 H0556: 1, H0650: 1, S0001: 1, S0376: 1, H0574: 1, S0346: 1, H0328: 1, L0649: 1, H0689: 1, H0660: 1, L0752: 1 and H0445: 1. | | | |
| 183 | HHPTC55 | 1106390 | 193 | 2 - 676 | 1093 | Ile-26 to Arg-44, Ser-85 to Leu-93, Ala-97 to Gln-104, Ile-141 to Gly-149, Asp-172 to Gly-177. | AR089: 1, AR061: 1 H0265: 1, H0556: 1, H0477: 1, S0112: 1 and L0794: 1. | | | |
| 184 | HJBBP54 | 907951 1195070 | 748 194 | 1 - 435 3 - 575 | 1648 1094 | Ala-18 to Arg-23, Phe-28 to Asn-33, Arg-79 to Lys-84, Arg-104 to Ser-112, Asn-181 to Thr-188. Ala-18 to Arg-23. | AR061: 193, AR089: 73 H0265: 1, H0050: 1, H0634: 1 and T0042: 1. | | | |
| 185 | HKAHB56 | 869621 1162649 | 749 195 | 3 - 575 674 - 1609 | 1649 1095 | Gln-1 to His-6, Pro-9 to Leu-16, Trp-41 to His-47, His-49 to Val-57, Arg-103 to Gln-110, Glu-119 to Lys-125, Gln-173 to Gln-180, Pro-216 to Arg-226, Ile-281 to Ser-287. | AR061: 0, AR089: 0 L0751: 3, L0747: 3, H0662: 2, H0641: 2, L0749: 2, L0758: 2, S0114: 1, H0638: 1, S0046: 1, H0427: 1, H0618: 1, H0424: 1, H0553: 1, H0032: 1, H0494: 1, S0450: 1, L0773: 1, L0804: 1, | | | |

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| 186 | HLDCI35 | 865298 | 750 | 3 - 1346 | 1650 | Pro-57 to Gln-69, Asn-71 to Phe-81. | L0653: 1, L0792: 1, L0666: 1, H0689: 1, H0435: 1, H0660: 1, H0521: 1, L0752: 1, L0755: 1, L0596: 1 and H0542: 1. | | |
| | | 1151490 | 196 | 66 - 725 | 1096 | Val-39 to Lys-47, Cys-81 to Trp-86, Arg-213 to Gly-218. | AR061: 3, AR089: 1 L0748: 7, L0791: 2, H0597: 1, H0509: 1, L0803: 1, L0804: 1 and L0581: 1. | | |
| 187 | HMCBU79 | 831356 | 751 | 66 - 725 | 1651 | Val-39 to Lys-47, Cys-81 to Trp-86. | | | |
| | | 1165318 | 197 | 1 - 987 | 1097 | Met-59 to Lys-70, Thr-134 to Arg-139, Gly-211 to Tyr-216, Asn-237 to Lys-256, Ser-264 to Asp-271, Ser-290 to Asp-302, Ser-309 to Arg-315, Asp-320 to Phe-325. | AR061: 8, AR089: 4 L0748: 4, H0306: 2, L0766: 2, L0659: 2, L0756: 2, L0758: 2, S0134: 1, S0418: 1, H0632: 1, H0486: 1, T0060: 1, L0021: 1, H0644: 1, T0067: 1, S0142: 1, L0638: 1, L0772: 1, L0800: 1, L0768: 1, L0775: 1, L0375: 1, L0655: 1, L0791: 1, L0663: 1, H0651: 1, S0330: 1, L0749: 1, L0779: 1, | | |

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| 188 | HNTRV07 | 856630 | 752 | 1 - 501 | 1652 | Met-62 to Lys-73, Thr-137 to Arg-142. | AR061: 1, AR089: 1 L0803: 5, L0665: 2, L0438: 2, L0758: 2, S0418: 1, L0717: 1, H0586: 1, H0622: 1, H0038: 1, L0662: 1, L0794: 1, L0783: 1, L0790: 1, L0664: 1, H0547: 1, H0519: 1, H0672: 1, H0539: 1, S0152: 1, L0740: 1, L0747: 1, L0777: 1 and S0242: 1. | L0759: 1 and H0542: 1. | | |
| 189 | HODEX10 | 952794 1104108 | 753 199 | 1 - 366 237 - 1 | 1653 1099 | Gln-15 to Lys-21, Arg-57 to His-72. | AR061: 6, AR089: 3 H0615: 5 | | | |
| 190 | HOGAQ10 | 926260 1222600 | 754 200 | 22 - 159 65 - 1069 | 1654 1100 | Met-1 to Arg-6, Ser-16 to Lys-29. | AR089: 1, AR061: 0 S0422: 4, L0750: 4, L0766: 3, L0794: 2, S0242: 2, H0542: 2, H0170: 1, S0116: 1, H0675: 1, H0497: 1, H0486: 1, H0013: 1, H0090: 1, H0040: 1, H0551: 1, L0649: 1, | | | |

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| 191 | HOSBW20 | 985056 | 201 | 1 - 927 | 1101 | 1655 | Asp-40 to Gln-60, Phe-99 to Ser-104, Ser-109 to Gln-117, Lys-123 to Lys-137, Asn-175 to Pro-181. | AR061: 3, AR089: 2 S0206: 2, L0439: 2, S0222: 1, S0003: 1, H0428: 1, L0766: 1 and L0438: 1. | L0606: 1, H0519: 1, H0435: 1, L0779: 1, L0593: 1 and H0543: 1. |
| 192 | HRADL60 | 1151310 | 202 | 2765 - 1203 | 1102 | 1656 | Val-41 to Asp-46, Met-64 to Arg-70, Arg-135 to Lys-146, Tyr-151 to Asn-157, Glu-167 to Ser-172. | AR089: 2, AR061: 1 L0777: 12, L0766: 9, L0803: 5, L0748: 5, L0752: 5, L0758: 5, L0759: 5, L0666: 4, L0794: 3, L0805: 3, L0743: 3, L0747: 3, S0222: 2, H0457: 2, S0003: 2, L0649: 2, L0804: 2, L0809: 2, L0663: 2, L0664: 2, | |

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| | H0539: 2, L0744: 2, L0740: 2, L0596: 2, L0362: 2, S0026: 2, H0624: 1, H0170: 1, T0049: 1, H0402: 1, H0638: 1, S0420: 1, L0454: 1, S0356: 1, S0360: 1, H0637: 1, H0393: 1, L0717: 1, H0486: 1, T0082: 1, L0163: 1, H0594: 1, H0266: 1, H0416: 1, H0328: 1, H0622: 1, T0006: 1, H0553: 1, H0674: 1, H0163: 1, H0038: 1, H0634: 1, H0616: 1, H0551: 1, H0625: 1, H0538: 1, L0598: 1, L0770: 1, L0646: 1, L0764: 1, L0662: 1, L0375: 1, L0515: 1, L0659: 1, L0783: 1, L0789: 1, L0791: 1, T0068: 1, H0520: 1, H0684: 1, H0658: 1, H0518: 1, S0013: 1, S0146: 1, H0555: 1, L0779: 1, L0780: 1, L0757: 1 and S0462: 1 | |
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| 193 | HSGSC29 | 1150837 | 757 | 68 - 1630 | 1657 | Val-41 to Asp-46, Met-64 to Arg-70, Arg-135 to Lys-146, Tyr-151 to Asn-157, Glu-167 to Ser-172. Val-19 to His-24, Gly-88 to Gly-93, Pro-156 to Arg-169. | AR089: 5, AR061: 5 H0255: 4, H0593: 3, H0620: 2, H0448: 2, H0254: 1, S0358: 1, H0208: 1, H0592: 1 and H0272: 1. | | |
| 194 | HTEDX38 | 1106208 | 758 | 327 - 749 | 1658 | Leu-13 to Tyr-18, Tyr-108 to Gly-113. | AR061: 8, AR089: 5 L0794: 4, L0766: 4, L0758: 4, H0624: 3, H0038: 3, S0007: 2, H0616: 2, L0770: 2, L0803: 2, H0144: 2, L0751: 2, L0747: 2, L0750: 2, H0170: 1, T0049: 1, S0376: 1, S0045: 1, H0553: 1, H0040: 1, T0042: 1, H0646: 1, L0768: 1, L0655: 1, L0787: 1, L0788: 1, L0666: 1, L0665: 1, H0520: 1, S0126: 1, H0435: 1, S0378: 1, L0720: 1, | | |

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| 195 | HTEJE15 | 920697 | 759 | 3 - 1436 | 1659 | Gln-124 to Arg-135, Ser-149 to Ser-154, Lys-161 to Ser-176, Ala-184 to Val-204, Pro-207 to His-216, Tyr-270 to Gln-281, Ser-300 to Tyr-327, Gly-330 to Asp-346, Gln-352 to Glu-367, Gly-380 to Ser-397, Gln-401 to Trp-409, Phe-420 to Tyr-435, Ala-453 to Ser-458. | H0555: 1, L0779: 1, L0777: 1 and S0192: 1. | | |
| | | 1102531 | 205 | 1 - 405 | 1105 | Arg-38 to Thr-48, Asp-107 to Thr-114, Ser-123 to Asp-135. | | | |
| 196 | HTOES03 | 908360 | 760 | 2 - 319 | 1660 | | AR061: 4, AR089: 1 L0758: 7, L0794: 4, H0038: 2 and L0791: 1. | | |
| | | 1150877 | 206 | 2 - 1186 | 1106 | Ala-1 to Ala-8, Ala-11 to Ser-22, Gln-86 to Ala-92, Asp-156 to Leu-167, Arg-169 to Arg-176, Glu-325 to Ala-332, Asp-354 to Leu-360, Ser-387 to Lys-395. | | | |
| | | 955814 | 761 | 3 - 1022 | 1661 | Arg-1 to His-8, Gln-27 to Ala-33, Asp-97 to Leu-108, | AR089: 1, AR061: 0 L0766: 7, H0561: 2, L0774: 2, L0777: 2, H0052: 1, H0264: 1, H0625: 1, L0761: 1, L0806: 1, L0776: 1, L0790: 1, L0793: 1, L0779: 1 and L0752: 1. | | |

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| 197 | HTOHS18 | 1193057 | 207 | 3 - 1070 | 1107 | Arg-110 to Arg-117, Glu-266 to Ala-273, Asp-295 to Leu-301, Ser-328 to Ala-340. Cys-10 to Gln-16, Gly-66 to Arg-72, Asp-170 to Trp-178, His-207 to Arg-212, Thr-265 to Lys-270, Lys-274 to Lys-285, Lys-306 to Gly-314, Phe-331 to Val-356. | AR061: 3, AR089: 1 L0777: 7, H0486: 3, L0659: 3, H0436: 2, L0731: 2, L0758: 2, H0171: 1, S0134: 1, H0657: 1, H0662: 1, L0717: 1, H0592: 1, H0485: 1, H0581: 1, H0264: 1, H0100: 1, H0633: 1, L0763: 1, L0770: 1, L0637: 1, L0772: 1, L0764: 1, L0662: 1, L0805: 1, L0776: 1, L0655: 1, L0783: 1, H0659: 1, L0612: 1, L0749: 1, L0750: 1 and H0352: 1. | | |
| 198 | HWAAX38 | 908347 943936 | 762 208 | 2 - 592 3 - 404 | 1662 1108 | Cys-5 to Gln-11. Ala-21 to Gln-27. | AR089: 5, AR061: 2 H0423: 6, H0556: 4, H0486: 4, H0271: 4, S0134: 3, H0657: 3, H0125: 3, S0278: 3, H0581: 3, L0768: 3, S0330: 3, H0134: 3, H0436: 3, H0445: 3, | | |

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| 199 | HMSFN70 | 1210794 | 209 | 1 - 921 | 1109 | Gly-25 to Arg-33, Glu-40 to Thr-55, Asp-125 to Lys-136, Val-174 to Pro-185, Pro-228 to Ala-235, Glu-270 to Gly-275, Pro-299 to Lys-307. | L0779: 1, L0755: 1 and H0136: 1. AR061: 4, AR089: 3 L0759: 7, L0731: 6, L0769: 4, L0766: 4, L0742: 3, L0751: 3, L0752: 3, H0624: 2, S6026: 2, L0770: 2, L0803: 2, L0774: 2, L0666: 2, H0670: 2, H0521: 2, L0754: 2, L0750: 2, L0777: 2, L0753: 2, L0757: 2, H0171: 1, H0650: 1, H0341: 1, H0675: 1, H0580: 1, H0574: 1, H0013: 1, H0052: 1, H0051: 1, H0083: 1, S6028: 1, S0003: 1, L0483: 1, H0644: 1, H0628: 1, H0038: 1, S0002: 1, L0772: 1, L0764: 1, L0768: 1, L0794: 1, L0806: 1, L0805: 1, L0776: 1, L0807: 1, L0656: 1, L0789: 1, H0689: 1, H0672: 1, H0555: 1, S0027: 1, L0756: 1, L0779: 1, L0755: 1 and | | | |
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| | | | | | | | | | L0758: 1. | | |
| 200 | HUSGB93 | 921879 1224029 | 763 210 | 1 - 921 363 - 983 | 1663 1110 | | | | AR089: 98, AR061: 8 S0126: 2, H0341: 1, H0412: 1, L0387: 1, L0766: 1, L0379: 1, L0559: 1, S0374: 1 and S0434: 1. | | |
| | | 923014 | 764 | 2 - 520 | 1664 | Arg-1 to Gly-8, Pro-18 to Gly-25, Thr-60 to Leu-67, Gly-107 to Thr-113. | | | | | |
| 201 | HELHL56 | 1164004 | 211 | 2 - 943 | 1111 | Ser-10 to Ser-16, Lys-226 to Trp-231, Thr-288 to Ser-300. | | | AR061: 4, AR089: 2 S0426: 3, L0766: 3, S0126: 2, S0282: 1, S0354: 1, S0376: 1, S0045: 1, H0486: 1, H0178: 1, S0003: 1, H0622: 1, H0591: 1, H0040: 1, H0551: 1, H0647: 1, L0761: 1, L0651: 1, S0152: 1, H0521: 1, H0522: 1, S0028: 1, L0754: 1, L0757: 1, L0592: 1 and H0542: 1. | | |
| | | 578441 | 765 | 2 - 307 | 1665 | Ser-10 to Ser-16, Phe-89 to Ser-97. | | | | | |
| 202 | HOENY85 | 1191756 | 212 | 2 - 1357 | 1112 | | | | AR061: 5, AR089: 2 S0354: 1, S0045: 1. | | |

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| 203 | HTEHI14 | 875830 | 766 | 2 - 664 | 1666 | Lys-133 to Trp-138, Thr-195 to Gln-206. | H0178: 1, H0622: 1, H0591: 1, H0040: 1, H0647: 1, L0766: 1, S0126: 1, S0152: 1, H0521: 1, S0028: 1, L0754: 1, L0592: 1 and H0542: 1. | AR089: 5, AR061: 5 H0038: 4 | | |
| | | 1102680 | 213 | 209 - 541 | 1113 | Asp-57 to Lys-62. | | | | |
| | | 526687 | 767 | 216 - 458 | 1667 | | | | | |
| 204 | HETDT70 | 1228235 | 214 | 1 - 588 | 1114 | Gly-33 to Asp-45, Ser-78 to Gly-85. | AR089: 153, AR061: 40 H0648: 138, L0666: 63, L0595: 48, L0662: 47, L0663: 47, S0360: 45, H0670: 44, H0659: 43, L0659: 41, L0526: 39, S0358: 37, L0664: 35, L0717: 31, L0775: 31, H0657: 30, L0750: 30, T0010: 29, L0655: 29, L0665: 27, H0543: 27, L0598: 23, H0672: 23, S0330: 23, H0170: 21, L0351: 21, L0520: 21, L0646: 19, L0521: 19, L0752: 19, S0380: 18, L0596: 18, L0361: | | | |

18, H0413: 17, L0593: 17, L0362: 17, L0500: 16, L0657: 16, S0374: 16, H0519: 15, L0483: 14, H0144: 14, L0747: 14, L0375: 13, H0436: 13, L0588: 13, S0418: 12, H0428: 12, L0748: 12, H0422: 12, S0376: 11, L0591: 11, S0114: 10, H0529: 10, H0547: 10, H0506: 10, H0686: 9, H0402: 9, H0486: 9, H0560: 9, S0002: 9, L0769: 9, L0638: 9, S0328: 9, S0378: 9, L0756: 9, L0605: 9, S0412: 9, S0212: 8, H0411: 8, H0581: 8, H0052: 8, H0553: 8, L0763: 8, L0497: 8, L0565: 8, L0602: 8, H0445: 8, H0352: 8, H0624: 7, H0497: 7, L0471: 7, H0087: 7, H0551: 7, H0412: 7, S0422: 7, L0651: 7, L0653: 7, L0517: 7, H0520: 7, S0192: 7, S0276: 7, H0685: 6, S0420: 6, H0013: 6,

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H0050: 6, H0355: 6,
 H0188: 6, H0059: 6,
 L0641: 6, L0522: 6,
 L0783: 6, H0435: 6,
 H0576: 6, L0589: 6,
 L0581: 6, L0599: 6,
 S0116: 5, S0356: 5,
 S0007: 5, S0045: 5,
 H0351: 5, H0597: 5,
 H0014: 5, S0388: 5,
 S0250: 5, H0625: 5,
 S0426: 5, L0637: 5,
 L0766: 5, L0518: 5,
 L0782: 5, H0682: 5,
 H0658: 5, H0539: 5,
 L0759: 5, H0423: 5,
 H0650: 4, H0125: 4,
 S0354: 4, H0580: 4,
 S0046: 4, S0414: 4,
 T0060: 4, H0421: 4,
 H0545: 4, H0046: 4,
 H0009: 4, H0012: 4,
 H0057: 4, H0688: 4,
 T0006: 4, H0674: 4,
 H0163: 4, H0591: 4,
 H0509: 4, L0648: 4,
 L0767: 4, L0768: 4,
 L0650: 4, L0527: 4,
 L0530: 4, H0518: 4,
 L0592: 4, L0608: 4,
 L0603: 4, S0026: 4,

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S0242: 4, H0542: 4,
H0395: 3, S0040: 3,
H0341: 3, S0282: 3,
H0255: 3, H0663: 3,
H0662: 3, H0306: 3,
H0208: 3, H0393: 3,
H0640: 3, H0586: 3,
H0587: 3, H0150: 3,
H0123: 3, H0024: 3,
S0316: 3, H0617: 3,
H0032: 3, H0068: 3,
H0135: 3, H0561: 3,
L0625: 3, L0501: 3,
L0606: 3, L0519: 3,
L0438: 3, H0660: 3,
H0134: 3, H0187: 3,
S0392: 3, L0754: 3,
L0731: 3, H0667: 3,
H0171: 2, H0394: 2,
S0342: 2, S0134: 2,
H0583: 2, H0656: 2,
L0416: 2, L0760: 2,
H0669: 2, H0661: 2,
S0444: 2, H0637: 2,
S0468: 2, H0619: 2,
H0441: 2, H0333: 2,
H0485: 2, T0039: 2,
H0318: 2, H0546: 2,
N0006: 2, H0565: 2,
H0242: 2, T0003: 2,
H0015: 2, H0373: 2,

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H0222: 1, H0431: 1,
H0608: 1, H0611: 1,
H0610: 1, H0415: 1,
H0537: 1, H0438: 1,
H0612: 1, H0600: 1,
H0592: 1, H0642: 1,
H0643: 1, H0574: 1,
H0632: 1, H0559: 1
L0623: 1, T0040: 1,
L0586: 1, T0109: 1,
H0250: 1, H0635: 1,
H0427: 1, H0599: 1,
H0098: 1, H0575: 1,
T0082: 1, H0590: 1,
S0010: 1, T0048: 1,
T0071: 1, H0196: 1,
H0251: 1, L0033: 1,
H0309: 1, H0263: 1,
H0596: 1, H0231: 1,
H0041: 1, H0019: 1,
H0620: 1, H0154: 1,
H0051: 1, H0083: 1,
H0354: 1, H0266: 1,
S0334: 1, H0687: 1,
H0288: 1, H0286: 1,
S0312: 1, S0003: 1,
H0252: 1, H0328: 1,
H0030: 1, L0143: 1,
H0111: 1, H0166: 1,
H0673: 1, S0364: 1,
H0035: 1, H0598: 1.

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| | H0038: 1, H0040: 1, H0272: 1, H0268: 1, T0004: 1, H0079: 1, L0062: 1, H0100: 1, T0041: 1, T0042: 1, H0512: 1, S0015: 1, H0396: 1, S0382: 1, S0294: 1, L0065: 1, S0438: 1, S0150: 1, H0130: 1, H0641: 1, H0633: 1, H0646: 1, S0144: 1, S0142: 1, S0344: 1; S0208: 1, : 1, H0026: 1, L0640: 1, L0770: 1, L0667: 1, L0627: 1, L0772: 1, L0373: 1, L0372: 1, L0626: 1, L0794: 1, L0381: 1, L0499: 1, L0803: 1, L0804: 1, L0774: 1, L0376: 1, L0607: 1, L0629: 1, L0510: 1, L0513: 1, L0635: 1, L0382: 1, L0809: 1, L0545: 1, L0529: 1, L0647: 1, L0789: 1, L0532: 1, L0352: 1, H0689: 1, H0690: 1, H0683: 1, H0684: 1, L0355: 1, S0152: 1, S0004: 1, |
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| 205 | HPIAT34 | 936262 | 768 | 1 - 597 | 1668 | Gly-33 to Asp-45, Ser-78 to Gly-85. | S0190: 1, S0176: 1, S0146: 1, S0404: 1, H0555: 1, H0478: 1, H0479: 1, H0631: 1, S0037: 1, S0028: 1, L0741: 1, L0742: 1, L0744: 1, L0439: 1, L0745: 1, L0746: 1, L0757: 1, S0031: 1, H0343: 1, S0434: 1, L0597: 1, L0594: 1, L0601: 1, S0011: 1 and : 1. | | |
| | | 937999 | | | | | | | |
| 206 | HDPP041 | 1204324 | 216 | 102 - 1937 | 1116 | Arg-98 to Thr-104, Gln-117 to Lys-122, Tyr-250 to Leu-262, Leu-294 to Phe-304. | AR061: 7, AR089: 3 L0752: 3, L0748: 2, L0740: 2, L0731: 2, S0358: 1, H0438: 1, H0574: 1, H0046: 1, H0041: 1, H0272: 1, S0150: 1, L0794: 1, L0803: 1, L0804: 1, L0775: 1, L0661: 1, L0789: 1, H0672: 1, H0539: 1 and L0758: 1. AR089: 0, AR061: 0 L0439: 13, L0748: 7, H0591: 4, L0770: 4, L0779: 4, L0777: 4. | | |

H0622: 3, H0560: 3,
L0794: 3, L0518: 3,
L0752: 3, L0588: 3,
S0376: 2, H0013: 2,
H0581: 2, H0231: 2,
L0163: 2, H0090: 2,
H0623: 2, S0142: 2,
L0772: 2, L0766: 2,
L0655: 2, L0665: 2,
H0144: 2, L0565: 2,
L0352: 2, H0689: 2,
L0758: 2, L0759: 2,
H0542: 2, T0002: 1,
H0657: 1, S0116: 1,
H0341: 1, S0212: 1,
H0638: 1, S0007: 1,
H0619: 1, H0411: 1,
S0278: 1, H0497: 1,
H0486: 1, H0635: 1,
H0156: 1, H0046: 1,
H0051: 1, S6028: 1,
S0003: 1, H0551: 1,
H0509: 1, H0641: 1,
H0646: 1, S0002: 1,
H0529: 1, L0640: 1,
L0639: 1, L0768: 1,
L0804: 1, L0651: 1,
L0659: 1, L0809: 1,
L0788: 1, L0663: 1,
H0701: 1, H0703: 1,
S0374: 1, H0547: 1,

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| 207 | HMSHI83 | 1204709 | 217 | 2 - 1720 | 1117 | Arg-59 to Thr-65, Gln-78 to Lys-83, Tyr-211 to Leu-223, Leu-255 to Phe-265, Gly-320 to Lys-328, Arg-343 to Phe-354, Pro-533 to Ser-553. | Arg-98 to Thr-104, Gln-117 to Lys-122. | H0522: 1, H0555: 1, H0478: 1, L0744: 1, L0750: 1, L0731: 1, H0423: 1 and S0424: 1. | | |
| | | 963126 | 769 | 102 - 620 | 1669 | | | AR089: 4, AR061: 3 L0439: 13, L0748: 7, H0591: 4, L0770: 4, L0779: 4, L0777: 4, H0622: 3, H0560: 3, L0794: 3, L0518: 3, L0752: 3, L0588: 3, S0376: 2, H0013: 2, H0581: 2, H0231: 2, L0163: 2, H0090: 2, H0623: 2, S0142: 2, L0772: 2, L0766: 2, L0655: 2, L0665: 2, H0144: 2, L0565: 2, L0352: 2, H0689: 2, L0758: 2, L0759: 2, H0542: 2, T0002: 1, H0657: 1, S0116: 1, H0341: 1, S0212: 1, H0638: 1, S0007: 1, H0619: 1, H0411: 1, S0278: 1, H0497: 1, H0486: 1, H0635: 1, H0156: 1, H0046: 1. | | |

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|-----|---------|--------|-----|----------|------|---|--|--|--|
| 208 | HTEPM45 | 963083 | 770 | 2 - 841 | 1670 | Arg-59 to Thr-65, Gln-78 to Lys-83, Tyr-211 to Leu-223, Glu-257 to Lys-262. | H0051: 1, S6028: 1, S0003: 1, H0551: 1, H0509: 1, H0641: 1, H0646: 1, S0002: 1, H0529: 1, L0640: 1, L0639: 1, L0768: 1, L0804: 1, L0651: 1, L0659: 1, L0809: 1, L0788: 1, L0663: 1, H0701: 1, H0703: 1, S0374: 1, H0547: 1, H0522: 1, H0555: 1, H0478: 1, L0744: 1, L0750: 1, L0731: 1, H0423: 1 and S0424: 1. | | |
| | | 952389 | 218 | 3 - 1229 | 1118 | Arg-1 to Cys-9, Tyr-47 to Leu-59, Leu-91 to Phe-101, Gly-156 to Lys-164, Arg-179 to Phe-190, Pro-369 to Ser-389. | AR089: 9, AR061: 7 H0486: 102, S0360: 76, L0598: 39, H0251: 35, L0659: 32, H0144: 32, H0013: 31, H0624: 28, H0024: 26, H0050: 25, L0471: 25, L0662: 22, L0748: 22, H0619: 20, H0123: 20, S0003: 18, H0031: 15, H0170: 14, H0124: 14, H0328: | | |

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| 13, L0750: 13, H0644: | |
| 12, S0126: 12, S0028: | |
| 11, L0757: 11, S0196: | |
| 11, H0587: 10, S0214: | |
| 10, L0589: 10, S0040: 9, | |
| H0622: 9, L0731: 9, | |
| H0171: 8, S0356: 8, | |
| L0717: 8, H0586: 8, | |
| H0620: 8, H0252: 8, | |
| H0551: 8, H0352: 8, | |
| H0661: 7, H0081: 7, | |
| L0747: 7, L0755: 7, | |
| S0358: 6, H0598: 6, | |
| L0646: 6, L0771: 6, | |
| S3014: 6, H0343: 6, | |
| H0595: 6, S0212: 5, | |
| H0329: 5, H0208: 5, | |
| H0574: 5, H0316: 5, | |
| H0100: 5, L0666: 5, | |
| L0565: 5, H0658: 5, | |
| S0390: 5, S0027: 5, | |
| S0011: 5, S0192: 5, | |
| S0194: 5, S0376: 4, | |
| H0575: 4, H0039: 4, | |
| H0628: 4, H0090: 4, : 4, | |
| L0663: 4, L0664: 4, | |
| S0374: 4, S0380: 4, | |
| L0744: 4, S0242: 4, | |
| H0295: 3, H0645: 3, | |
| H0411: 3, H0546: 3, | |
| H0012: 3, S0250: 3, | |

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L0768: 3, L0375: 3,
H0684: 3, H0672: 3,
S0332: 3, L0754: 3,
H0294: 2, H0663: 2,
H0592: 2, S0005: 2,
H0333: 2, H0632: 2,
H0485: 2, T0060: 2,
H0599: 2, H0309: 2,
H0544: 2, H0545: 2,
H0041: 2, H0375: 2,
H0553: 2, L0142: 2,
H0647: 2, L0776: 2,
L0665: 2, H0648: 2,
S0330: 2, S0378: 2,
S0206: 2, S0032: 2,
L0751: 2, H0668: 2,
S0384: 2, H0506: 2,
L0615: 1, S0342: 1,
H0381: 1, S0116: 1,
S0001: 1, H0664: 1,
H0125: 1, S0354: 1,
T0008: 1, H0640: 1,
H0370: 1, H0391: 1,
T0039: 1, H0101: 1,
H0245: 1, H0156: 1,
L0021: 1, H0122: 1,
H0318: 1, H0231: 1,
H0049: 1, T0003: 1,
H0051: 1, H0286: 1,
H0364: 1, H0428: 1,
T0023: 1, L0143: 1,

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| Pro-312 to Leu-327, Pro-332 to Thr-338, His-412 to Gln-418, Val-470 to Phe-475. | L0752: 4, H0624: 3, H0090: 3, H0560: 3, L0769: 3, L0768: 3, L0783: 3, L0755: 3, H0171: 2, S0007: 2, H0497: 2, H0486: 2, H0052: 2, H0316: 2, H0494: 2, S0150: 2, L0776: 2, L0655: 2, L0659: 2, L0665: 2, H0547: 2, S0027: 2, L0756: 2, L0759: 2, L0588: 2, H0136: 2, H0542: 2, H0341: 1, H0664: 1, H0458: 1, H0125: 1, S0418: 1, S0376: 1, S0360: 1, H0489: 1, S0132: 1, S0300: 1, H0351: 1, H0601: 1, H0632: 1, H0013: 1, H0244: 1, H0069: 1, H0427: 1, H0318: 1, H0581: 1, H0421: 1, H0204: 1, H0327: 1, H0046: 1, S0388: 1, S0051: 1, S6028: 1, H0687: 1, S0003: 1, H0252: 1, H0615: 1, H0428: 1, T0006: 1, H0553: 1, L0055: 1, H0038: 1 |
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| 211 | HHEDC90 | 1226157 | 221 | 192 - 3269 | 1121 | Arg-8 to Lys-19, Gln-75 to Pro-84, Ser-112 to Ser-120, Asn-132 to Glu-138, Ala-159 to Lys-172, Arg-217 to Gln-223, Asp-254 to Ser-259, Glu-297 to Gln-304, Pro-385 to Lys-395, Tyr-422 to Leu-427, Gln-438 to Glu-446, Arg-500 to Leu-510, Leu-555 to Thr-562, Pro-568 to Asp-573, Ser-648 to Ser-653, Ala-770 to Gly-777, Trp-803 to Leu-808, Leu-833 to Trp-843, Ala-851 to Thr-856, Lys-866 to Gly-873, Leu-904 to Arg-911, Arg-953 to Arg-961, Cys-973 to Arg-978, Pro-1003 to Arg-1016. | AR061: 3, AR089: 3, H0250: 4, L0766: 4, H0543: 4, H0559: 3, H0306: 2, H0635: 2, H0641: 2, H0521: 2, L0779: 2, H0542: 2, H0423: 2, H0556: 1, H0402: 1, L0468: 1, H0190: 1, H0069: 1, H0581: 1, H0087: 1, T0041: 1, L0761: 1, L0768: 1, S0053: 1, H0672: 1 and H0422: 1. | | |
| | | 911447 | 774 | 1 - 687 | 1674 | His-1 to Leu-7, Leu-52 to Thr-59, Pro-65 to Asp-70, Ser-145 to Ser-150. | | | |
| 212 | HNBRB59 | 685902 | 222 | 28 - 339 | 1122 | Ala-47 to Gly-55. | H0026: 1, L0560: 1, L0378: 1 and H0595: 1. | | |

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| 213 | HNBNB116 | 965414 | 775 | 1 - 237 | 1675 | Asn-17 to Lys-25, Arg-40 to Glu-46, Lys-64 to His-75. Arg-12 to Val-20, Gln-43 to Glu-51. | AR089: 1, AR061: 1 H0521: 4, H0650: 3, H0677: 3, H0656: 2, H0069: 2, H0581: 2, H0542: 2, H0423: 2, H0255: 1, L0539: 1, S0358: 1, H0575: 1, H0457: 1, H0083: 1, H0063: 1, H0560: 1, S0002: 1, H0529: 1, H0697: 1, H0543: 1 and H0422: 1. |
| 214 | HUJCL61 | 1223496 | 224 | 135 - 2861 | 1124 | Arg-8 to Lys-19, Gln-75 to Pro-84, Ser-112 to Ser-120, Asn-132 to Glu-138, Ala-159 to Lys-172, Arg-217 to Gln-223, Asp-254 to Ser-259, Glu-297 to Gln-304, Pro-385 to Lys-395, Tyr-422 to Leu-427, Gln-438 to Glu-446, Arg-500 to Leu-510, Leu-555 to Thr-562, Pro-568 to Asp-573, Ser-648 to Ser-653 | AR089: 3, AR061: 1 L0766: 6, H0521: 6, H0250: 5, H0543: 5, H0559: 4, H0581: 4, L0761: 4, L0779: 4, H0542: 4, H0650: 3, H0306: 3, H0069: 3, H0023: 3, H0423: 3, H0422: 3, H0677: 3, H0656: 2, H0255: 2, H0257: 2, H0635: 2, H0560: 2, H0641: 2, L0789: 2, L0777: 2, H0556: 1, H0402: 1, L0539: 1, S0358: 1 |

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| 215 | HWLRC68 | 911432 | 776 | 116 - 715 | 1676 | Arg-8 to Lys-19, Gln-75 to Pro-84, Ser-112 to Ser-120. | Ala-770 to Gly-777, Trp-803 to Leu-808, Leu-833 to Trp-843, Ala-851 to Thr-856, Gln-863 to Trp-873, Cys-883 to Arg-901. | L0468: 1, H0190: 1, H0575: 1, H0457: 1, H0083: 1, H0063: 1, H0087: 1, T0041: 1, S0002: 1, H0695: 1, H0529: 1, L0764: 1, L0768: 1, S0053: 1, H0697: 1, H0702: 1, H0658: 1, H0672: 1, L0731: 1 and H0445: 1. | | |
| | | 1089187 | 225 | 33 - 1238 | 1125 | | | AR061: 2, AR089: 1 S0360: 1, S0132: 1 and H0412: 1. | | |
| 216 | HFXFH42 | 911481 1228147 | 777 226 | 210 - 548 383 - 724 | 1677 1126 | Glu-65 to Arg-72. Ser-36 to Lys-42, Ala-70 to Gln-86. | | AR061: 1, AR089: 0 L0770: 2, L0803: 2, L0439: 2, L0740: 2, L0731: 2, S0001: 1, H0373: 1, L0638: 1, L0766: 1, L0655: 1, L0787: 1, L0788: 1, L0745: 1, L0755: 1 and L0366: 1. | | |
| 217 | HEQAN73 | 713795 958912 | 778 227 | 220 - 399 12 - 878 | 1678 1127 | Glu-28 to Phe-33, His-47 to Ser-53. | | AR089: 6, AR061: 3 L0439: 6, L0804: 4. | | |

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| | | | | | | | | L0794: 3, L0756: 3, L0779: 3, H0125: 2, H0599: 2, H0544: 2, H0046: 2, L0764: 2, L0766: 2, L0803: 2, L0438: 2, H0521: 2, L0731: 2, S0452: 2, S0045: 1, S0046: 1, H0549: 1, H0575: 1, H0374: 1, H0194: 1, H0545: 1, H0083: 1, S0003: 1, H0328: 1, T0006: 1, H0623: 1, L0761: 1, L0768: 1, L0775: 1, L0806: 1, L0805: 1, L0666: 1, L0663: 1, H0520: 1, H0519: 1, H0682: 1, S0380: 1, H0445: 1, H0542: 1 and H0506: 1. | | |
| 218 | HSLFS31 | 1106294 | 228 | 575 - 252 | 1128 | Met-1 to Glu-14, Thr-73 to Glu-81, Ala-86 to Ile-96. | AR061: 5, AR089: 3 S0044: 1 and S0028: 1. | | | |
| 219 | HELK56 | 921511 | 779 | 3 - 215 | 1679 | Glu-31 to Leu-36. | AR061: 3, AR089: 1 S0045: 1 | | | |
| | | 1103702 | 229 | 575 - 33 | 1129 | | | | | |
| | | 925698 | 780 | 129 - 788 | 1680 | | | | | |
| 220 | HAMFW05 | 957586 | 230 | 1 - 558 | 1130 | Asp-1 to Gly-9, Asp-86 to Glu-91, Pro-97 to Gly-103. | AR089: 13, AR061: 2 H0521: 6, L0757: 5, L0749: 4 L0779: 4 | | | |

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| Lys-115 to Asn-121, Pro-159 to Arg-166, Pro-168 to His-173. | H0620: 3, S0040: 2, S0342: 2, H0305: 2, S0418: 2, S0132: 2, H0551: 2, H0412: 2, S0344: 2, L0776: 2, L0659: 2, L0740: 2, L0747: 2, L0752: 2, H0542: 2, T0049: 1, H0656: 1, S0001: 1, H0306: 1, S0360: 1, S0046: 1, H0619: 1, H0370: 1, H0559: 1, H0590: 1, H0266: 1, H0288: 1, H0286: 1, H0252: 1, H0213: 1, H0673: 1, H0116: 1, H0433: 1, H0623: 1, H0560: 1, H0652: 1, S0002: 1, H0529: 1, L0762: 1, L0763: 1, L0772: 1, L0646: 1, L0764: 1, L0765: 1, L0662: 1, L0766: 1, L0526: 1, L0783: 1, L0789: 1, S0126: 1, H0435: 1, H0539: 1, S0152: 1, H0522: 1, H0555: 1, S014: 1, L0777: 1, L0731: 1, L0758: 1, S0031: 1, S0011: 1 and S0446: 1. |
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| 221 | HTEDG81 | 1193054 | 231 | 70 - 828 | 1131 | Leu-58 to Val-64, Lys-120 to Phe-132, Tyr-150 to Thr-157, Glu-178 to Glu-183, Arg-217 to Leu-222, Glu-236 to Ser-252. | AR089: 2, AR061: 2, H0038: 3, L0758: 2, H0616: 1 and T0042: 1. | | |
| 222 | HAMGO24 | 772995 | 781 | 75 - 497 | 1681 | Leu-58 to Val-64. | AR089: 2, AR061: 1, L0766: 9, L0742: 6, S0358: 3, L0803: 3, H0521: 3, L0777: 3, L0758: 3, H0413: 2, S0466: 2, L0775: 2, L0666: 2, L0779: 2, L0752: 2, S0360: 1, H0393: 1, H0587: 1, H0486: 1, H0013: 1, H0069: 1, H0575: 1, H0052: 1, H0545: 1, H0510: 1, S0003: 1, H0553: 1, H0560: 1, H0509: 1, S0422: 1, L0598: 1, L0762: 1, L0794: 1, L0804: 1, L0664: 1, H0519: 1, H0522: 1, L0755: 1, S0031: 1 and H0653: 1. | | |
| | | 943287 | 232 | 2 - 550 | 1132 | Asp-10 to Phe-15, Ser-57 to Leu-62, Lys-77 to Val-83. | | | |
| 223 | HMWBH91 | 1193044 | 233 | 249 - 1298 | 1133 | Glu-13 to Ser-19, Lys-45 to Pro-50, Ser-89 to Gly-96, | AR061: 2, AR089: 2, L0777: 8, L0779: 5, L0646: 3, L0803: 3, | | |

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| 224 | HOECH19 | 965639 | 234 | 140 - 934 | 1134 | Pro-314 to Phe-319, Asn-322 to Asn-327, Gly-366 to Lys-372, Ile-388 to Ala-395, Glu-402 to Arg-407. Ala-5 to Ser-11, Ser-101 to Asn-112. | AR061: 8, AR089: 3 L0759: 9, L0758: 8, L0439: 5, L0163: 4, L0809: 4, L0779: 4, L0770: 3, L0750: 3, L0777: 3, H0063: 2, L0794: 2, L0766: 2, L0659: 2, L0438: 2, S0126: 2, H0666: 2, L0747: 2, L0757: 2, H0542: 2, H0656: 1, L0785: 1, H0574: 1, L0105: 1, H0687: 1, H0644: 1, H0038: 1, H0616: 1, L0475: 1, L0520: 1, L0769: 1, L0646: 1, L0764: 1, L0803: 1, L0774: 1, L0775: 1, L0776: 1, L0655: 1, L0559: 1, L0663: 1, L0665: 1, H0684: 1, S0152: 1, H0555: 1, L0751: 1, L0749: 1, L0755: 1, L0731: 1, S0434: 1 | | |
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| 225 | HSRAA80 | 1121919 | 235 | 2 - 379 | 1135 | Ile-1 to Cys-10, Arg-95 to Arg-104. | S0242: 1, H0543: 1, H0422: 1 and S0412: 1. AR061: 150, AR089: 93 S0011: 1 | | |
| | | 937640 | 783 | 2 - 325 | 1683 | Ile-1 to Cys-10, Arg-95 to Phe-106. | | | |
| 226 | HHEDF50 | 1174682 | 236 | 5 - 502 | 1136 | | AR089: 3, AR061: 1 H0542: 40, H0543: 10, H0580: 4, H0592: 4, H0510: 4, H0593: 4, H0521: 4, H0551: 3, H0509: 3, H0519: 3, H0650: 2, H0586: 2, H0587: 2, H0544: 2, H0546: 2, H0545: 2, H0522: 2, H0555: 2, H0583: 1, H0602: 1, H0581: 1, H0488: 1, H0689: 1, H0528: 1 and H0694: 1. | | |
| | | 974396 | 784 | 5 - 502 | 1684 | | | | |
| 227 | HHEMK34 | 974395 | 237 | 29 - 277 | 1137 | Gln-1 to Val-8. | AR061: 1, AR089: 1 H0542: 40, H0543: 10, H0580: 4, H0592: 4, H0510: 4, H0593: 4, H0521: 4, H0551: 3, H0509: 3, H0519: 3, H0650: 2, H0586: 2, H0587: 2, H0544: 2, | | |

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| | | | | | | | | | H0546: 2, H0545: 2, H0522: 2, H0555: 2, H0583: 1, H0602: 1, H0581: 1, H0488: 1, H0689: 1, H0528: 1 and H0694: 1. | | | |
| 228 | HMAGK69 | 1105451 | 238 | 556 - 77 | 1138 | Ala-3 to Gly-9, Lys-36 to Glu-42, Ala-49 to Glu-55, Ser-90 to Gln-102, His-134 to Trp-139. | | | AR089: 2, AR061: 1, S0278: 1 and S0052: 1. | | | |
| | | 723186 | 785 | 31 - 417 | 1685 | Arg-1 to Ser-6, Lys-23 to Glu-29, Ala-36 to Glu-42, Ser-77 to Gln-89. | | | | | | |
| 229 | HNGNW52 | 1132300 | 239 | 939 - 43 | 1139 | Leu-25 to Ala-31, Ala-102 to Ala-108, Ser-285 to Gly-290. | | | AR089: 37, AR061: 13 S0050: 1, H0031: 1, S0428: 1, S0028: 1, S0031: 1 and S0260: 1. | | | |
| | | 883074 | 786 | 38 - 1009 | 1686 | | | | | | | |
| 230 | H6EDK67 | 974775 | 240 | 75 - 668 | 1140 | Lys-29 to Arg-34, Glu-121 to Asp-126, Lys-132 to Asp-155. | | | AR089: 24, AR061: 7 L0777: 5, S0116: 3, L0809: 3, H0696: 3, H0423: 3, S0282: 2, S0354: 2, H0083: 2, H0316: 2, L0763: 2, L0767: 2, L0805: 2, L0776: 2, L0779: 2, S0114: 1, H0657: 1, H0656: 1, S0358: 1, | | | |

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| 231 | HWBCS43 | 1151532 | 241 | 125 - 880 | 1141 | Ser-13 to Gln-29, Pro-31 to Lys-38, Asp-82 to Gln-90, His-175 to Gly-180, Thr-186 to Gly-202. | S0360: 1, H0340: 1, S0046: 1, H0619: 1, H0455: 1, H0333: 1, H0574: 1, H0559: 1, T0109: 1, H0156: 1, L0021: 1, T0074: 1, H0318: 1, S0474: 1, S0049: 1, H0327: 1, H0530: 1, H0615: 1, H0553: 1, H0673: 1, H0059: 1, L0065: 1, H0207: 1, L0520: 1, L0769: 1, L0761: 1, L0521: 1, L0774: 1, L0655: 1, L0659: 1, L0526: 1, L0666: 1, L0664: 1, H0659: 1, H0518: 1, S0176: 1, H0478: 1, L0748: 1, L0750: 1, L0755: 1, L0731: 1, S0436: 1, L0608: 1, L0362: 1, S0026: 1 and S0242: 1. AR089: 16, AR061: 3 L0747: 11, L0731: 8, L0740: 7, L0361: 6, H0657: 5, H0658: 5, H0542: 5, H0494: 4, L0770: 4, L0772: 4, L0766: 4, L0748: 4. | | |
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| | L0757: 4, L0758: 4, H0580: 3, H0587: 3, H0551: 3, H0413: 3, L0666: 3, H0144: 3, S0374: 3, H0547: 3, H0648: 3, L0750: 3, L0756: 3, L0581: 3, H0423: 3, H0624: 2, H0170: 2, H0656: 2, H0341: 2, H0663: 2, H0638: 2, S0360: 2, S0046: 2, H0486: 2, H0318: 2, H0373: 2, H0266: 2, S0003: 2, H0252: 2, T0041: 2, H0529: 2, L0763: 2, L0769: 2, L0764: 2, L0768: 2, L0774: 2, L0526: 2, L0664: 2, H0689: 2, H0670: 2, H0672: 2, S0380: 2, H0521: 2, S0028: 2, L0751: 2, L0754: 2, H0543: 2, S0424: 2, H0556: 1, S0040: 1, H0294: 1, T0049: 1, L0808: 1, S0116: 1, S0212: 1, S0418: 1, S0354: 1, S0358: 1, H0637: 1, S0045: 1, S0222: 1, H0602: 1 | | | | | |
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| | H0586: 1, H0574: 1, H0485: 1, H0069: 1, H0427: 1, S0280: 1, H0156: 1, H0003: 1, H0581: 1, H0530: 1, H0545: 1, L0471: 1, H0012: 1, H0024: 1, S0362: 1, H0355: 1, H0375: 1, H0416: 1, H0687: 1, S0214: 1, H0328: 1, H0615: 1, H0535: 1, H0031: 1, H0673: 1, H0124: 1, H0488: 1, H0056: 1, H0100: 1, H0625: 1, L0065: 1, H0641: 1, S0002: 1, L0520: 1, L0762: 1, L0637: 1, L0761: 1, L0630: 1, L0646: 1, L0648: 1, L0363: 1, L0364: 1, L0389: 1, L0804: 1, L0775: 1, L0375: 1, L0806: 1, L0527: 1, L0512: 1, L0659: 1, L0518: 1, L0783: 1, L0384: 1, L0382: 1, L0543: 1, L0367: 1, L0787: 1, L0663: 1, L0665: 1, H0698: 1, H0593: 1, H0365: 1 | | | | | | |
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| | | | | | | | | H0660: 1, S0330: 1, H0539: 1, S0136: 1, H0522: 1, H0694: 1, H0555: 1, H0576: 1, S0390: 1, S3014: 1, S0027: 1, S0032: 1, L0779: 1, L0752: 1, L0755: 1, L0588: 1, L0591: 1, S0011: 1, S0026: 1, S0276: 1, H0422: 1 and H0506: 1. | | |
| 232 | HCE3H71 | 961681 | 787 | 285 - 737 | 1687 | Asp-29 to Gln-37. | | AR089: 14, AR061: 10 L0439: 12, L0438: 5, L0741: 4, H0052: 2, H0009: 2, L0769: 2, L0794: 2, H0229: 1, H0572: 1, L0770: 1, L0796: 1, L0789: 1 and L0786: 1. | | |
| 233 | HOFMS43 | 947973 | 243 | 3 - 359 | 1143 | Asp-1 to Asp-17, Pro-61 to Asn-66, Tyr-84 to Tyr-90, Ser-103 to Trp-110. | | AR051: 15, AR050: 9, AR089: 7, AR061: 5, AR054: 1 H0415: 1 | | |
| 234 | HOVCO14 | 947999 | 244 | 3 - 539 | 1144 | Arg-78 to His-85, Leu-99 to Lys-104, Lys-123 to His-132, Ser-157 to Pro-174. | | AR089: 3, AR061: 2 S6016: 1 and H0428: 1. | | |
| 235 | HTOBE75 | 1161571 | 245 | 3 - 1067 | 1145 | Gly-53 to Thr-60, Ser-72 to Ser-88. | | AR061: 2, AR089: 1 H0038: 3, L0748: 3. | | |

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|-----|---------|--------|-----|----------|------|---|---|--|--|--|
| 236 | HCMSL08 | 591896 | 788 | 1 - 414 | 1688 | Gly-1 to Thr-10, Ala-14 to Gly-19, Pro-52 to Val-57, Pro-85 to Gln-95, Lys-198 to His-204, Pro-254 to Glu-260, Glu-269 to Ser-282, Glu-302 to Gly-307, Asp-320 to Asp-326, Asp-373 to Ser-380, Ile-396 to Asp-407. | L0659: 2, L0743: 2, L0744: 2, H0486: 1, H0421: 1, H0024: 1, H0031: 1, H0272: 1, L0662: 1, L0384: 1, L0809: 1 and L0779: 1. | | | 104770, 107670, 110700, 135940, 145001, 146790, 152445, 152445, 159001, 174000, 179755, 182860, 182860, 182860, 191315, 230800, 230800, 266200, 600897, 601105, 601412, 601652, 602491 |
| | | 898203 | 246 | 1 - 1221 | 1146 | AR051: 86, AR054: 73, AR050: 67, AR089: 10, AR061: 5 H0706: 8, S0366: 5, S0364: 4, L0485: 4, L0604: 4, L0777: 3, L0623: 2, S0362: 2, H0373: 2, L0520: 2, L0747: 2, H0624: 1, H0619: 1, H0550: 1, H0196: 1, L0646: 1, L0809: 1, H0693: 1, S0328: 1 and H0214: 1. | AR051: 86, AR054: 73, AR050: 67, AR089: 10, AR061: 5 H0706: 8, S0366: 5, S0364: 4, L0485: 4, L0604: 4, L0777: 3, L0623: 2, S0362: 2, H0373: 2, L0520: 2, L0747: 2, H0624: 1, H0619: 1, H0550: 1, H0196: 1, L0646: 1, L0809: 1, H0693: 1, S0328: 1 and H0214: 1. | | | |

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| | | 959176 | 789 | 1372 - 569 | 1689 | Lys-59 to His-65, Pro-115 to Glu-121, Glu-130 to Ser-143, Glu-163 to Gly-168, Asp-181 to Asp-187, Asp-234 to Ser-241, Ile-257 to Asp-268. | | | | | |
| 237 | HDPBS64 | 846624 | 247 | 2 - 685 | 1147 | Phe-7 to Pro-15, Trp-34 to Gly-40. | AR089: 1, AR061: 0 S0222: 1, S0002: 1, L0804: 1, L0663: 1 and H0521: 1. | | | | |
| 238 | HDTBR50 | 846630 | 248 | 130 - 342 | 1148 | Ala-2 to Glu-7, Arg-50 to Glu-58. | AR089: 41, AR061: 4 H0486: 2 | | | | |
| 239 | HTDAB17 | 890384 | 249 | 3 - 605 | 1149 | Asp-1 to Gly-14, Ala-60 to Lys-71, Gln-101 to Glu-118. | AR089: 1, AR061: 0 L0747: 28, L0588: 22, L0757: 19, H0251: 15, S0358: 14, S0045: 13, L0731: 12, H0551: 10, H0412: 10, L0771: 10, L0748: 9, L0758: 9, H0506: 9, H0556: 8, S0046: 8, H0622: 8, H0013: 7, H0623: 7, L0662: 7, S0192: 7, S0003: 6, L0659: 6, L0666: 6, S0328: 6, L0439: 6, L0750: 6, L0759: 6, L0599: 6, L0608: 6, S0040: 5, S0360: 5, H0581: 5, | 6p24-p23 | 125264, 134570, 600511, 601556 | | |

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| | H0529: 5, L0763: 5, L0764: 5, L0664: 5, H0144: 5, S0026: 5, S0212: 4, H0486: 4, H0674: 4, L0776: 4, S0126: 4, H0672: 4, S0136: 4, L0752: 4, H0624: 3, S0420: 3, H0599: 3, H0004: 3, H0266: 3, H0615: 3, H0031: 3, H0553: 3, H0591: 3, H0264: 3, H0413: 3, H0494: 3, S0210: 3, L0770: 3, L0806: 3, H0519: 3, H0435: 3, L0740: 3, L0751: 3, L0749: 3, H0170: 2, H0657: 2, H0656: 2, S0356: 2, S0408: 2, H0619: 2, H0393: 2, H0333: 2, T0040: 2, H0427: 2, S0280: 2, H0156: 2, H0318: 2, H0596: 2, T0110: 2, H0545: 2, H0046: 2, H0009: 2, H0050: 2, L0471: 2, H0188: 2, H0328: 2, H0428: 2, L0483: 2, H0644: 2, H0038: 2, S0426: 2, L0772: 2, | |
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| H0057: 1, H0051: 1, H0083: 1, H0510: 1, H0687: 1, H0288: 1, S0022: 1, H0039: 1, H0030: 1, H0628: 1, H0166: 1, H0212: 1, H0135: 1, H0163: 1, H0090: 1, H0040: 1, H0634: 1, H0087: 1, H0477: 1, H0488: 1, H0433: 1, H0268: 1, H0269: 1, H0056: 1, S0038: 1, H0100: 1, H0429: 1, S0450: 1, H0132: 1, H0633: 1, S0472: 1, H0647: 1, H0646: 1, H0652: 1, S0344: 1, L0640: 1, L0371: 1, L0372: 1, L0374: 1, L0767: 1, L0768: 1, L0364: 1, L0794: 1, L0650: 1, L0375: 1, L0378: 1, L0606: 1, L0656: 1, L0783: 1, L0647: 1, S0374: 1, T0068: 1, L0438: 1, H0547: 1, H0689: 1, H0711: 1, H0684: 1, H0659: 1, H0670: 1, H0648: 1, S0330: 1, S0378: 1, |
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| | | | | | | | | | S0380: 1, H0709: 1, S0146: 1, S3012: 1, S0037: 1, S0206: 1, L0742: 1, L0744: 1, L0755: 1, H0707: 1, S0434: 1, S0436: 1, L0584: 1, L0593: 1, L0362: 1, S0011: 1, S0424: 1 and H0293: 1. | | |
| 240 | HABAE22 | 1227053 | 250 | 1086 - 1 | 1150 | Gly-8 to Gly-13, Ala-76 to Ala-81, Arg-154 to Gly-159, Arg-338 to Pro-349. | | | AR089: 1, AR061: 0 H0617: 10, L0743: 4, S0358: 3, H0618: 3, H0052: 3, H0687: 3, H0135: 3, H0494: 3, L0646: 3, L0750: 3, L0731: 3, L0757: 3, L0601: 3, H0484: 2, H0662: 2, S0418: 2, H0549: 2, H0599: 2, H0150: 2, H0181: 2, H0087: 2, H0412: 2, H0529: 2, L0769: 2, L0649: 2, L0775: 2, L0663: 2, H0547: 2, L0742: 2, H0543: 2, H0556: 1, H0686: 1, H0685: 1, S0134: 1, S0218: 1, H0483: 1, H0661: 1, H0664: 1, S0360: 1, S0046: 1, | | |

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| S0278: 1, S0222: 1, H0441: 1, H0438: 1, H0592: 1, H0257: 1, H0486: 1, H0250: 1, H0042: 1, H0575: 1, H0253: 1, H0505: 1, H0318: 1, H0581: 1, H0545: 1, L0163: 1, S0051: 1, H0266: 1, S0338: 1, H0428: 1, H0039: 1, H0031: 1, H0606: 1, S0366: 1, S0036: 1, H0551: 1, H0059: 1, H0561: 1, H0647: 1, S0142: 1, H0538: 1, S0002: 1, S0426: 1, L0770: 1, L0374: 1, L0771: 1, L0768: 1, L0774: 1, L0378: 1, L0776: 1, L0807: 1, L0512: 1, L0659: 1, L0666: 1, H0435: 1, H0672: 1, S0328: 1, S0152: 1, L0744: 1, L0751: 1, L0747: 1, L0749: 1, L0786: 1, L0755: 1, L0759: 1, S0434: 1, L0592: 1, L0604: 1, L0594: 1, L0595: 1, H0667: 1 and H0542: 1 |
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| 241 | HE9MI70 | 1217048 | 965314 | 790 | 3 - 767 | 1690 | Arg-1 to Ala-6, Glu-28 to Ala-34, Gln-41 to Gly-70, Ala-161 to Phe-168, Lys-180 to Arg-191, His-193 to Leu-198, Glu-216 to Asp-227. Gln-1 to Arg-8, Glu-68 to Glu-74, Tyr-93 to Gln-99, Gly-119 to Val-124, Glu-149 to His-154, Asp-178 to Asp-183, Pro-231 to Leu-241. | AR089: 21, AR061: 7 S0126: 3, L0163: 2, S0426: 2, H0547: 2, L0439: 2, L0751: 2, S0418: 1, S0468: 1, L0471: 1, S0051: 1, H0673: 1, L0637: 1, L0794: 1, L0663: 1, H0144: 1, S0027: 1, L0752: 1, L0757: 1 and H0444: 1. |
| 242 | HHFDK15 | 1147850 | 953319 | 791 | 1 - 684 | 1691 | Ser-24 to Ser-38, Pro-72 to Gly-97, Lys-146 to His-153, Ser-173 to Ser-182, Leu-192 to Gln-201. | AR061: 72, AR089: 44 L0438: 7, L0805: 4, L0779: 4, L0439: 3, H0619: 2, S0010: 2, L0766: 2, L0809: 2, L0754: 2, L0755: 2, L0594: 2, L0601: 2, H0422: 2, S0430: 1, H0656: 1, H0484: 1, S0360: 1, S0222: 1, H0581: 1, H0327: 1. |

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| 243 | HOSNZ11 | 854734 | 792 | 3 - 380 | 1692 | Gly-17 to Thr-26, Glu-93 to Asp-101, Arg-117 to Ala-125. | H0050: 1, L0471: 1, H0644: 1, L0768: 1, L0794: 1, L0774: 1, L0776: 1, L0636: 1, L0787: 1, L0665: 1, H0672: 1, H0696: 1, L0751: 1, L0780: 1, L0608: 1, S0194: 1 and H0677: 1. | |
| | | 1162664 | 253 | 2 - 481 | 1153 | Gln-10 to Thr-18, Ser-40 to Lys-47, Lys-59 to Lys-64, Lys-73 to Leu-82, Asp-145 to Thr-160. | AR061: 6, AR089: 2 L0439: 4, L0770: 2, L0794: 2, L0438: 2, L0740: 2, H0599: 1, T0082: 1, S0003: 1, H0644: 1, L0639: 1, S3014: 1, S0028: 1, S0206: 1, L0756: 1, L0779: 1 and L0752: 1. | |
| 244 | HTAEW05 | 965875 | 793 | 3 - 461 | 1693 | Ala-27 to Ala-36, Glu-41 to Asp-48, Asp-84 to Lys-92, Ala-140 to Glu-145, Leu-168 to Glu-173, Gln-213 to Ser-218. | AR089: 11, AR061: 7 L0766: 3, L0617: 1, H0069: 1, H0318: 1, H0050: 1, S0250: 1, L0804: 1, L0663: 1, L0750: 1, L0786: 1, L0752: 1 and L0592: 1. | |
| | | 1151514 | 254 | 98 - 817 | 1154 | Ala-27 to Ala-36, Glu-41 to Asp-48, Asp-84 to Lys-92, Ala-140 to Glu-145, Leu-168 to Glu-173, Gln-213 to Ser-218. | | |
| | | 838562 | 794 | 91 - 615 | 1694 | Ala-27 to Ala-36 | | |

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|-----|---------|---------|-----|------------|------|--|--|----|--|--|
| 245 | HTTKN45 | 1181807 | 255 | 249 - 1772 | 1155 | Glu-41 to Asp-48, Asp-84 to Lys-92, Ala-140 to Glu-145. Gln-2 to Ala-11, Pro-23 to Gly-32, Lys-38 to Gln-52, Thr-57 to Ser-64, Thr-72 to Ala-78, Asp-88 to Asp-93, Lys-107 to Gln-126. | AR089: 6, AR061: 6 H0634: 4, H0547: 3, H0521: 3, H0224: 2, H0208: 2, H0040: 2, H0529: 2, H0144: 2, H0656: 1, S0356: 1, H0600: 1, T0039: 1, H0013: 1, T0110: 1, H0046: 1, H0266: 1, H0032: 1, H0090: 1, H0038: 1, H0551: 1, T0041: 1, T0042: 1, H0509: 1, S0150: 1, H0539: 1, H0518: 1, S0152: 1, S0011: 1 and H0136: 1. | | | |
| 246 | HUSJN62 | 923146 | 256 | 1189 - 353 | 1156 | Gly-14 to Glu-38, Asn-90 to Lys-100, Lys-150 to Val-158, Ser-166 to Gly-175. Gln-3 to Gly-9, Ala-100 to Phe-107, Lys-119 to Arg-130, His-132 to Leu-137, Glu-155 to Ser-167, Val-194 to Pro-204, Gly-225 to Ile-233. | AR089: 1, AR061: 0 H0617: 10, L0743: 4, S0358: 3, H0618: 3, H0052: 3, H0687: 3, H0135: 3, H0494: 3, L0646: 3, L0750: 3, L0731: 3, L0757: 3, | 16 | | |

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| | L0601: 3, H0484: 2, H0662: 2, S0418: 2, H0549: 2, H0599: 2, H0150: 2, H0181: 2, H0087: 2, H0412: 2, H0529: 2, L0769: 2, L0649: 2, L0775: 2, L0663: 2, H0547: 2, L0742: 2, H0543: 2, H0556: 1, H0686: 1, H0685: 1, S0134: 1, S0218: 1, H0483: 1, H0661: 1, H0664: 1, S0360: 1, S0046: 1, S0278: 1, S0222: 1, H0441: 1, H0438: 1, H0592: 1, H0257: 1, H0486: 1, H0250: 1, H0042: 1, H0575: 1, H0253: 1, H0505: 1, H0318: 1, H0581: 1, H0545: 1, L0163: 1, S0051: 1, H0266: 1, S0338: 1, H0428: 1, H0039: 1, H0031: 1, H0606: 1, S0366: 1, S0036: 1, H0551: 1, H0059: 1, H0561: 1, H0647: 1, S0142: 1, H0538: 1, S0002: 1, S0426: 1, L0770: 1, | | | | | | |
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| 247 | HTEIU92 | 1102681 | 257 | 1 - 564 | 1157 | Asp-5 to Arg-13, Thr-37 to Ser-45, Ser-131 to Pro-137, Glu-154 to His-160, Lys-162 to Arg-168, Ile-180 to Asn-185. | L0374: 1, L0771: 1, L0768: 1, L0774: 1, L0378: 1, L0776: 1, L0807: 1, L0512: 1, L0659: 1, L0666: 1, H0435: 1, H0672: 1, S0328: 1, S0152: 1, L0744: 1, L0751: 1, L0747: 1, L0749: 1, L0786: 1, L0755: 1, L0759: 1, S0434: 1, L0592: 1, L0604: 1, L0594: 1, L0595: 1, H0667: 1 and H0542: 1. | | |
| | | 870652 | 796 | 1 - 339 | 1696 | Asp-5 to Arg-13, Thr-37 to Ser-45. | AR061: 3, AR089: 1 H0038: 3 | | |
| 248 | HAQMD86 | 1105267 | 258 | 1 - 1911 | 1158 | | AR061: 1, AR089: 1 L0748: 8, L0439: 8, L0766: 5, L0803: 5, L0749: 4, L0731: 4, S0046: 3, L0794: 3, L0805: 3, L0809: 3, L0666: 3, L0438: 3, H0543: 3, S0376: 2, | | |

S0007: 2, H0373: 2,
H0644: 2, L0455: 2,
L0598: 2, L0769: 2,
L0646: 2, L0804: 2,
L0774: 2, L0789: 2,
H0521: 2, H0627: 2,
L0743: 2, L0740: 2,
L0754: 2, L0595: 2,
H0170: 1, H0656: 1,
S0116: 1, H0638: 1,
H0125: 1, S0418: 1,
S0420: 1, S0356: 1,
S0360: 1, H0619: 1,
H0411: 1, H0586: 1,
H0486: 1, H0013: 1,
L0021: 1, H0098: 1,
H0575: 1, H0004: 1,
H0052: 1, S028: 1,
H0266: 1, H0674: 1,
H0090: 1, H0063: 1,
H0641: 1, H0646: 1,
L0640: 1, L0763: 1,
L0770: 1, L0761: 1,
L0373: 1, L0800: 1,
L0641: 1, L0764: 1,
L0773: 1, L0783: 1,
H0144: 1, L0565: 1,
H0593: 1, H0659: 1,
H0658: 1, H0522: 1,
S0392: 1, L0751: 1,
L0747: 1, L0777: 1

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| 249 | HBJTG02 | 961459 1151462 | 797 259 | 2 - 1912 501 - 1418 | 1697 1159 | Tyr-1 to Gly-6. Arg-12 to Tyr-23, Ser-93 to Thr-98, Lys-108 to Ser-113, Met-124 to Trp-129, Asp-173 to Ser-181, Pro-208 to Leu-213, Met-226 to Ser-231, Thr-250 to Pro-256, Glu-263 to Glu-273, Gln-301 to Arg-306. | AR089: 79, AR061: 26 L0002: 1, H0156: 1, L0021: 1, H0318: 1, H0561: 1, L0662: 1, L0794: 1, L0766: 1, S0026: 1, H0542: 1 and H0506: 1. | | L0755: 1, L0757: 1, L0759: 1, S0026: 1, S0242: 1 and H0542: 1. |
| 250 | HBJUN65 | 919508 1151463 | 798 260 | 2 - 1087 2 - 532 | 1698 1160 | Lys-49 to Thr-61, Ser-75 to Val-92, Phe-96 to Pro-124, Leu-139 to Ile-146. Lys-47 to Thr-59, Ser-73 to Val-90, Phe-94 to Pro-122, Leu-137 to Ile-144, Ile-197 to Trp-205, Glu-219 to Gly-228. Gly-7 to Tyr-15. | AR061: 8, AR089: 4 S0426: 2, S0126: 2, H0318: 1 and H0050: 1. | | |
| 251 | HBMUI35 | 1195500 | 261 | 2117 - 288 | 1161 | | AR089: 8, AR061: 8 L0439: 13, L0438: 4, H0046: 3, L0663: 3, H0556: 2, H0023: 2, T0010: 2, L0769: 2. | | |

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| 252 | HCEBP60 | 956041 | 800 | 627 - 253 | 1700 | Asp-7 to Glu-28, Ser-42 to Asp-69, Gln-79 to Asp-102, Leu-105 to Cys-112. | AR061: 7, AR089: 5 H0052: 3, H0135: 3, L0794: 3, L0439: 3, L0749: 3, H0583: 2. | L0655: 2, H0436: 2, L0743: 2, L0744: 2, L0748: 2, L0754: 2, L0747: 2, L0731: 2, L0759: 2, L0605: 2, S0116: 1, S0418: 1, H0619: 1, H0261: 1, S0222: 1, H0333: 1, H0492: 1, H0599: 1, H0052: 1, H0178: 1, H0050: 1, H0620: 1, H0179: 1, H0674: 1, S0364: 1, H0708: 1, H0100: 1, S0440: 1, S0142: 1, L0762: 1, L0796: 1, L0761: 1, L0521: 1, L0767: 1, L0766: 1, L0805: 1, L0652: 1, L0659: 1, L0783: 1, L0809: 1, L0665: 1, L0352: 1, H0660: 1, H0555: 1, L0749: 1, L0756: 1, L0777: 1, L0758: 1, L0595: 1 and H0542: 1. |
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| 253 | HFGMA55 | 1150870 | 263 | 1 - 444 | 1163 | Phe-6 to Glu-15, Asp-21 to Leu-33, Met-141 to Cys-147. | AR061: 1, AR089: 1 L0439: 13, L0438: 4, H0046: 3, L0663: 3, H0556: 2, H0023: 2, T0010: 2, L0769: 2, L0655: 2, H0436: 2, L0743: 2, L0744: 2, L0748: 2, L0754: 2, L0747: 2, L0731: 2, L0759: 2, L0605: 2, S0116: 1, S0418: 1, H0619: 1, H0261: 1, S0222: 1, H0333: 1, H0492: 1, H0599: 1, H0052: 1, H0178: 1, H0050: 1, H0620: 1, H0179: 1, H0674: 1, S0364: 1, H0708: 1, H0100: 1, S0440: 1, S0142: 1, L0762: 1, L0796: 1, L0761: 1, L0521: 1, L0767: 1, L0766: 1, L0805: 1, L0652: 1, L0659: 1, L0783: 1, L0809: 1, L0665: 1, L0352: 1, H0660: 1, H0555: 1, L0749: 1, L0756: 1, L0777: 1, L0758: 1, L0595: 1 and H0542: 1. | | |
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| 254 | HLHTE91 | 858681 | 802 | 3 - 416 | 1702 | Thr-5 to Glu-13, Asp-19 to Leu-31. | AR050: 526, AR054: 486, AR051: 283, AR089: 1, AR061: 1 L0439: 5, L0662: 4, H0543: 4, L0766: 3, L0665: 3, L0751: 3, L0777: 3, H0618: 2, H0052: 2, H0024: 2, L0666: 2, H0265: 1, S0212: 1, H0580: 1, H0208: 1, H0393: 1, H0549: 1, H0550: 1, S0222: 1, H0333: 1, H0559: 1, H0486: 1, T0114: 1, S0049: 1, H0041: 1, H0083: 1, H0615: 1, L0055: 1, H0135: 1, H0038: 1, H0634: 1, H0616: 1, H0413: 1, L0370: 1, L0770: 1, L0800: 1, L0768: 1, L0794: 1, L0803: 1, L0804: 1, L0653: 1, L0658: 1, L0789: 1, H0520: 1, H0660: 1, S0044: 1, S0146: 1, L0743: 1, L0740: 1, L0749: 1, |
| | | 789603 | 264 | 1 - 1203 | 1164 | | |

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| | | | | | | | | | L0750: 1, L0779: 1, L0752: 1, L0755: 1, L0731: 1 and H0423: 1. | | |
| | | 868803 | 803 | 3 - 1151 | 1703 | | | Leu-16 to Lys-21, Arg-30 to Pro-36, Ser-44 to Thr-49, Arg-136 to Arg-150, Leu-160 to Cys-173, Glu-223 to Gly-228, Gly-241 to Gln-249, Ala-260 to Gly-265, Ile-334 to Thr-349, Arg-364 to Glu-371. | | | |
| | | 969604 | 804 | 618 - 355 | 1704 | | | | | | |
| 255 | HL YFI58 | 1151495 | 265 | 2 - 625 | 1165 | | | Glu-9 to Ser-17, Phe-25 to Ala-34, Thr-43 to Asn-53, Met-172 to Gln-177. | AR061: 2, AR089: 1 L0777: 5, H0662: 3, H0251: 3, L0752: 3, L0759: 3, L0593: 3, L0771: 2, L0766: 2, L0666: 2, H0436: 2, L0745: 2, L0747: 2, L0779: 2, L0758: 2, H0650: 1, H0638: 1, S0358: 1, L0717: 1, H0586: 1, H0024: 1, H0373: 1, S0388: 1, S0051: 1, H0266: 1, S0003: 1, H0031: 1, H0551: 1, T0067: 1, S0422: 1, L0520: 1. | | |

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| 257 | HSLJ146 | 997643 | 267 | 1 - 540 | 1167 | Lys-457 to Pro-470, Gly-478 to Gln-483, Phe-519 to Cys-533. | Lys-1 to Gly-14, Gly-23 to Met-43, Ala-87 to Pro-99, Ile-101 to Ile-121, Gln-126 to Val-135, Val-139 to Cys-147. | AR089: 1, AR061: 0 H0521: 1 and S0390: 1. | | | |
| | | 883028 | 807 | 1 - 1551 | 1707 | | Lys-1 to Gly-14, Gly-23 to Ser-40. | | | | |
| 258 | HTFOK70 | 1151518 | 268 | 1 - 609 | 1168 | Ser-18 to Arg-25, Leu-45 to Pro-62, Gln-67 to Ala-72, Arg-143 to Gln-158, His-194 to Glu-203. | | AR061: 0, AR089: 0 H0617: 2, L0589: 2, S0420: 1, S0046: 1, H0575: 1, H0251: 1, H0616: 1, L0775: 1, L0651: 1, L0665: 1, L0748: 1, L0754: 1, L0731: 1, L0758: 1 and S0424: 1. | | | |
| | | 914561 | 808 | 179 - 616 | 1708 | | Cys-10 to Lys-27, Arg-86 to Gln-101, His-137 to Glu-146. | | | | |
| 259 | HUSXO71 | 1164014 | 269 | 3 - 317 | 1169 | Ala-30 to Pro-36, Glu-59 to Thr-71, Ser-77 to Leu-90. | | AR089: 14, AR061: 7 H0641: 4, L0596: 4, H0422: 4, L0768: 3, L0779: 3, L0758: 3, T0049: 2, H0486: 2, H0521: 2, H0522: 2, L0748: 2, L0747: 2, | | | |

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| | | | | | | | | L0777: 2, L0608: 2, L0601: 2, L0617: 1, H0497: 1, H0581: 1, H0544: 1, L0471: 1, H0687: 1, H0553: 1, H0090: 1, H0477: 1, H0413: 1, L0372: 1, L0774: 1, L0806: 1, L0659: 1, L0809: 1, L0789: 1, H0658: 1, H0648: 1, H0518: 1, L0750: 1, L0752: 1, L0731: 1, L0759: 1, L0590: 1 and H0423: 1. | | | |
| 260 | HWBDP39 | 1223498 | 809 | 648 - 1514 | 1709 | Arg-1 to Gly-7, Leu-9 to Ser-16, Arg-25 to Cys-35. | | | | AR089: 2, AR061: 1 L0439: 26, L0748: 22, L0744: 7, L0803: 6, L0805: 6, L0750: 6, H0013: 4, L0809: 4, L0766: 3, L0731: 3, L0758: 3, L0759: 3, H0624: 2, H0171: 2, H0156: 2, L0157: 2, L0471: 2, H0266: 2, H0059: 2, S0002: 2, H0529: 2, L0667: 2, L0800: 2, L0776: 2, | |

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| Gln-566 to Asn-577, Ser-614 to Cys-622, Phe-643 to His-648, Gln-658 to Phe-682, Asn-700 to Glu-729, Leu-737 to Asp-745. | L0659: 2, H0144: 2, L0740: 2, L0747: 2, L0752: 2, T0002: 1, H0650: 1, H0657: 1, L0425: 1, L0481: 1, S0418: 1, H0580: 1, H0351: 1, H0587: 1, H0333: 1, S0010: 1, S0346: 1, H0581: 1, H0596: 1, H0597: 1, H0457: 1, H0086: 1, H0172: 1, H0014: 1, H0373: 1, T0010: 1, H0083: 1, S0003: 1, H0328: 1, H0615: 1, H0119: 1, H0644: 1, S0366: 1, H0090: 1, H0038: 1, H0538: 1, L0770: 1, L0646: 1, L0374: 1, L0662: 1, L0768: 1, L0794: 1, L0804: 1, L0774: 1, L0789: 1, L0532: 1, L0666: 1, H0547: 1, H0519: 1, H0666: 1, S0152: 1, H0696: 1, H0555: 1, L0356: 1, L0749: 1, L0779: 1, S0260: 1, H0445: 1, S0434: 1, L0604: 1, L0601: 1, S0192: 1, |
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| 261 | HKMMQ73 | 810403 | 810 | 2 - 394 | 1710 | Glu-19 to Gln-29, Arg-48 to Ser-53, Glu-57 to Lys-73. | AR051: 19, AR050: 9, AR054: 8 H0431: 1, H0096: 1, L0659: 1 and H0506: 1. | S0194: 1, H0542: 1, H0543: 1 and H0352: 1. | |
| 262 | HVV BK72 | 840459 | 271 | 1 - 417 | 1171 | Gly-1 to Glu-6, Pro-18 to Lys-26, Glu-29 to Gly-36, Leu-104 to Ser-111, Asn-123 to Gly-130, His-134 to Lys-139. | | | |
| | | 949559 | 811 | 66 - 257 | 1711 | Ser-7 to Lys-29. | | | |
| | | 1179755 | 272 | 557 - 3 | 1172 | | AR061: 1, AR089: 1 H0038: 1, H0672: 1 and L0758: 1. | | |
| 263 | H7TXB52 | 933167 | 812 | 2 - 397 | 1712 | Glu-38 to Lys-43, Gly-125 to Thr-132. | | | |
| | | 981972 | 273 | 165 - 1322 | 1173 | | AR089: 1, AR061: 0 L0731: 6, H0012: 5, L0803: 4, S0028: 4, H0497: 3, H0581: 3, H0561: 3, L0769: 3, S0418: 2, H0599: 2, L0770: 2, L0771: 2, S0266: 2, L0757: 2, L0591: 2, L0594: 2, L0362: 2, H0668: 2, H0542: 2, H0171: 1, S6024: 1, H0341: 1, H0483: 1, H0663: 1, | | |

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| 264 | HDPY71 | 910910 1217205 | 813 274 | 165 - 1322 1365 - 661 | 1713 1174 | Gly-92 to Pro-97, Cys-107 to Gln-131, Pro-139 to Ala-147, Pro-149 to Arg-160, Thr-194 to Pro-206. | AR050: 58, AR054: 53, AR051: 41, AR089: 1, AR061: 0 H0644: 2, H0265: 1, S0001: 1, S0358: 1, H0431: 1, T0039: 1, H0575: 1, S0010: 1, H0052: 1, H0263: 1, H0051: 1, H0416: 1, H0212: 1, L0796: 1 | | |
| | | | | | | | H0125: 1, S0045: 1, H0369: 1, T0039: 1, T0109: 1, H0250: 1, H0635: 1, H0620: 1, H0083: 1, H0266: 1, S0003: 1, H0628: 1, H0032: 1, H0100: 1, T0041: 1, L0641: 1, L0775: 1, L0776: 1, L0655: 1, L0606: 1, L0659: 1, L0809: 1, L0367: 1, L0789: 1, L0663: 1, H0144: 1, S0148: 1, H0519: 1, S0126: 1, H0478: 1, L0751: 1, L0750: 1, L0756: 1, L0759: 1, H0444: 1, S0196: 1 and H0543: 1. | | |

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| | | | | | | | | | S0378: 1, H0521: 1, H0522: 1, S3014: 1, S0027: 1 and L0747: 1. | | | |
| 265 | HGOCA12 | 971345 | 814 | 441 - 806 | 1714 | Arg-85 to Lys-92, Leu-102 to Gln-115. | | | AR061: 210, AR089: 110 L0758: 3, S0364: 2, L0747: 2, S0278: 1, L0622: 1, H0018: 1, L0783: 1, L0809: 1, L0791: 1 and L0759: 1. | | | |
| 266 | HHCI29 | 971583 | 815 | 518 - 240 | 1715 | | | | | | | |
| 267 | HODGC61 | 1077517 | 276 | 1 - 2073 | 1176 | | | | | | | |
| | | 916885 | 816 | 2 - 574 | 1716 | | | | | | | |
| 268 | HBXGQ52 | 973449 | 277 | 43 - 324 | 1177 | Thr-50 to Gln-57. | | | AR061: 8, AR089: 5 H0615: 3 | | | |
| | | 1229467 | 278 | 2 - 1003 | 1178 | Gln-20 to Ser-28, Lys-31 to Arg-38, Asn-81 to His-93, Asn-148 to Asp-155, Met-182 to Gly-189, Pro-236 to Arg-243, Ala-258 to Ala-263, Pro-298 to Cys-304, Val-325 to Ala-333. | | | AR089: 4, AR061: 2 H0438: 3 and S0260: 1. | | | |
| 269 | HE2JS39 | 576093 | 817 | 1 - 291 | 1717 | | | | | | | |
| | | 1121932 | 279 | 790 - 2 | 1179 | Arg-1 to Lys-10, Gly-171 to Leu-176, Arg-217 to Arg-222, | | | AR089: 15, AR061: 10 L0750: 9, L0754: 5, L0779: 5, L0755: 4, | | | |

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| | | | | | | Glu-226 to Glu-232, Leu-257 to Ser-262. | | | L0360: 4, S0330: 3, L0747: 3, L0749: 2, L0777: 2, H0624: 1, H0650: 1, H0656: 1, S0376: 1, H0550: 1, H0592: 1, L0638: 1, H0689: 1, H0660: 1, L0731: 1, L0757: 1, L0759: 1 and L0359: 1. | |
| 270 | HE7SH21 | 957854 960302 | 818 280 | 51 - 716 3 - 1124 | 1718 1180 | Gly-1 to Gly-6. Pro-11 to Ser-20, Ala-35 to Pro-41, Gln-88 to Trp-95, Arg-111 to Asp-119. | | | AR089: 1, AR061: 0 L0439: 5, L0592: 3, H0052: 2, L0438: 2, L0741: 2, L0747: 2, S0001: 1, L0005: 1, S0007: 1, H0101: 1, L0109: 1, H0009: 1, H0051: 1, L0769: 1, L0594: 1 and L0595: 1. | |
| 271 | HMI AO23 | 1103488 | 281 | 2 - 478 | 1181 | Val-20 to Gln-36, Arg-67 to Gln-78, Pro-154 to Phe-159. | | | AR061: 4, AR089: 3 H0038: 2, L0439: 2, H0013: 1, S0010: 1, S6028: 1, H0090: 1, H0560: 1 and L0438: 1. | |
| 272 | HELDW45 | 944301 | 282 | 2 - 397 3 - 512 | 1719 1182 | Asn-1 to Gln-9, Arg-40 to Glu-51. Arg-6 to Gln-13, Thr-44 to Ser-50, Pro-145 to Asn-168. | | | AR089: 820, AR061: 90 S0045: 1, S0278: 1, H0617: 1 and S0044: 1. | |

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| 273 | HSRBB31 | 1121889 | 283 | 3 - 509 | 1183 | Tyr-14 to Cys-23, Arg-41 to Lys-46, Ser-53 to Asp-74, Glu-106 to Gln-116, Ser-129 to Leu-135. | AR089: 8, AR061: 8 H0038: 3, S0418: 1, S0132: 1, H0261: 1, H0574: 1, H0046: 1, S0364: 1, S0011: 1 and S0192: 1. | | |
| | | 958210 | 820 | 795 - 1676 | 1720 | | | | |
| 274 | HTEOW39 | 1151517 | 284 | 2 - 514 | 1184 | Gly-40 to Val-46, His-66 to Ser-72, Trp-83 to Gly-88, Trp-143 to Gly-149. | AR089: 17, AR061: 14 H0616: 2 | | |
| | | 870566 | 821 | 2 - 445 | 1721 | Gly-38 to Val-44. | | | |
| 275 | HE2PE32 | 1106571 | 285 | 1 - 468 | 1185 | Ala-76 to Gly-82, Thr-98 to Leu-105, Glu-126 to Ala-132. | AR089: 0, AR061: 0 H0013: 3, H0271: 2 and H0171: 1. | | |
| | | 524511 | 822 | 2 - 289 | 1722 | | | | |
| 276 | HSIDW39 | 1211446 | 286 | 2 - 748 | 1186 | | AR051: 12, AR054: 9, AR061: 5, AR089: 2, AR050: 0 H0036: 2, H0590: 2, S0354: 1, H0510: 1 and L0748: 1. | | |
| | | 775139 | 823 | 1 - 501 | 1723 | | | | |
| | | 830774 | 824 | 12 - 419 | 1724 | Glu-40 to Trp-57, Tyr-59 to Phe-64, Glu-91 to Arg-99, Asp-106 to Arg-114. | | | |
| 277 | HPMLD30 | 1226192 | 287 | 20 - 1666 | 1187 | Val-22 to Asp-27, Gly-37 to Gln-42, Thr-48 to Glu-54, | AR089: 1, AR061: 0 H0624: 1, S0626: 1, S0278: 1, S0051: 1, | | |

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| 278 | HOEKP17 | 937414 1204712 | 825 288 | 6 - 521 1 - 897 | 1725 1188 | Lys-61 to Pro-68, Ser-80 to Ser-89, Asp-96 to Phe-101, Leu-146 to Asp-153, Asp-169 to Val-174, Lys-219 to Gly-234, Leu-241 to Gln-247, Asp-269 to Ala-278, Asn-281 to Trp-289. | H0416: 1, H0644: 1, S0052: 1, S0053: 1, S0028: 1, S0032: 1, S0031: 1 and S0260: 1. | | |
| | | 937414 | 825 | 6 - 521 | 1725 | | | | |
| | | 1204712 | 288 | 1 - 897 | 1188 | Arg-12 to Arg-19, Trp-24 to Gly-35, Pro-42 to Arg-54, Ala-56 to Ser-61, Thr-78 to Asp-83, Thr-95 to Cys-108, Lys-174 to Lys-182, Lys-199 to Phe-210, Thr-222 to Ile-227. | AR061: 5, AR089: 2 L0754: 10, S0002: 3, L0766: 3, H0539: 3, H0370: 2, H0575: 2, H0581: 2, S0003: 2, H0038: 2, S0126: 2, L0751: 2, L0779: 2, L0758: 2, H0543: 2, H0664: 1, S0376: 1, H0639: 1, H0644: 1, L0055: 1, H0674: 1, H0090: 1, H0264: 1, H0561: 1, H0529: 1, L0640: 1, L0649: 1, L0803: 1, L0806: 1, H0684: 1, L0752: 1, L0753: 1, H0445: 1, L0608: 1 and L0362: 1. | | |
| | | 931049 | 826 | 3 - 1055 | 1726 | Arg-5 to Arg-12, Trp-17 to Gly-28, | | | |

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| 279 | HFXDP67 | 1228141 | 289 | 198 - 1205 | 1189 | Pro-35 to Arg-47, Ala-49 to Ser-54, Thr-71 to Asp-76, Thr-88 to Cys-101, Lys-167 to Lys-175, Lys-192 to Tyr-197. Pro-18 to Trp-24, Thr-32 to Asp-37, Arg-101 to Asp-107, Ala-148 to Ala-154, Gln-259 to Phe-264. | AR089: 0, AR061: 0 S0028: 4, S0126: 2, S0001: 1, S0282: 1, S0049: 1, S0050: 1, H0271: 1, H0388: 1 and S0390: 1. | | |
| 280 | HJABA59 | 526951 1199933 | 827 290 | 266 - 616 2 - 904 | 1727 1190 | Ala-21 to Ala-27. Pro-49 to Ala-59, Pro-127 to Phe-133, Arg-162 to Asn-173, Cys-183 to Asp-189, Lys-290 to Tyr-295. | AR061: 6, AR089: 3 L0755: 5, L0777: 4, L0752: 4, H0657: 3, S0016: 3, L0803: 3, S0330: 3, L0748: 3, L0740: 3, L0757: 3, H0622: 2, L0653: 2, L0666: 2, L0754: 2, L0779: 2, L0758: 2, S0040: 1, H0662: 1, L0481: 1, H0638: 1, S0418: 1, S0132: 1, H0393: 1, L0717: 1, H0586: 1, H0575: 1, H0052: 1, H0251: 1, L0157: 1, H0057: 1, S0003: 1, T0041: 1 | | |

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| 281 | HKIXB03 | 713642 | 828 | 366 - 902 | 1728 | Arg-6 to Phe-11, Arg-40 to Asn-51, Cys-61 to Asp-67. | L0794: 1, L0766: 1, L0522: 1, L0659: 1, L0789: 1, L0664: 1, L0665: 1, H0144: 1, S0374: 1, H0648: 1, L0439: 1, L0780: 1, L0731: 1, L0759: 1, L0591: 1 and S0192: 1. |
| | | 1129055 | 291 | 25 - 324 | 1191 | Arg-1 to Val-10, Ala-36 to Gly-47, Leu-66 to Ser-79. | AR061: 5, AR089: 4 H0441: 2 |
| 282 | HKMMF49 | 924636 1124742 | 829 292 | 21 - 371 1 - 600 | 1729 1192 | Arg-1 to Val-10. Gln-22 to Lys-28, Asp-69 to Leu-76, Phe-105 to Tyr-113, Leu-181 to Thr-190, Tyr-194 to Ser-200. | AR061: 4, AR089: 2 L0774: 4, L0803: 2, S0418: 1, S0360: 1, H0431: 1, L0157: 1, S0214: 1, H0551: 1, L0662: 1, L0767: 1, L0657: 1, L0659: 1, L0665: 1, H0660: 1 and L0777: 1. |
| | | 677960 | 830 | 1 - 600 | 1730 | Gln-22 to Lys-28, Asp-69 to Leu-76, Phe-105 to Tyr-113. | |
| 283 | HLD0G51 | 1151491 | 293 | 1 - 555 | 1193 | Tyr-87 to Pro-92, Gln-119 to Ser-124, Gln-152 to Tyr-160. | AR089: 1, AR061: 0 H0090: 2, L0794: 2, L0605: 2, L0485: 2. |

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| 284 | HSVAI25 | 918840 | 831 | 11 - 955 | 1731 | Lys-46 to His-53, Tyr-135 to Pro-140, Gln-167 to Ser-172, Glu-200 to Tyr-208, Gln-298 to Pro-305. | | | AR089: 12, AR061: 9 L0752: 2, H0309: 1, L0518: 1 and S0152: 1. | | |
| 285 | HSXCP56 | 577154 924635 | 832 295 | 99 - 245 213 - 962 | 1732 1195 | Glu-1 to Pro-9, Val-48 to Gly-55, Pro-70 to Thr-79, Arg-94 to Arg-99, Arg-111 to Thr-121, Thr-146 to Arg-154, Thr-179 to Asp-185, Pro-194 to Ser-200, Pro-215 to Thr-220. | | | AR061: 7, AR089: 5 L0768: 3, L0439: 3, H0618: 2, H0253: 2, H0620: 2, H0616: 2, H0561: 2, L0764: 2, L0766: 2, L0653: 2, H0539: 2, L0744: 2, L0747: 2, L0750: 2, H0318: 1, H0123: 1, H0081: 1, S0051: 1, S0036: 1, H0038: 1, L0630: 1, L0772: 1, L0771: 1, L0794: 1, L0806: 1, L0809: 1, L0666: 1, L0438: 1, | | |

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| 287 | HHFBU53 | 920940 | 1048855 | 833 | 297 | 3 - 347 | 1733 | Arg-19 to His-25. | H0622: 1, L0483: 1, H0644: 1, H0617: 1, H0673: 1, H0591: 1, H0087: 1, H0268: 1, H0269: 1, H0412: 1, H0056: 1, H0652: 1, L0769: 1, L0373: 1, L0764: 1, L0773: 1, L0521: 1, L0363: 1, L0649: 1, L0377: 1, L0388: 1, L0803: 1, L0775: 1, L0523: 1, L0806: 1, L0805: 1, L0653: 1, L0656: 1, L0558: 1, L0809: 1, L0647: 1, L0664: 1, L0565: 1, H0547: 1, H0435: 1, H0659: 1, H0670: 1, H0672: 1, S0380: 1, S0152: 1, H0704: 1, S3012: 1, S0206: 1, L0786: 1, L0758: 1, H0595: 1, L0589: 1, L0603: 1, H0665: 1, S0242: 1, S0276: 1, H0506: 1 and H0352: 1. | AR061: 4, AR089: 1 H0050: 1, L0748: 1, |
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| 288 | HTTDO45 | 837647 | 834 | 96 - 1061 | 1734 | Ser-138 to Ser-144. Ala-1 to Thr-17, Ser-106 to Ser-112. | L0439: 1 and H0506: 1. | | |
| | | 942505 | 298 | 327 - 1640 | 1198 | Val-1 to Gly-10, Arg-24 to Asp-36, Leu-225 to Trp-231, Val-249 to Met-258, Glu-262 to Thr-269, Val-279 to Gly-284, Asp-307 to Asn-313, Arg-411 to Lys-416. | AR061: 10, AR089: 3 L0803: 24, S0358: 13, S0360: 7, L0774: 6, L0769: 5, L0794: 5, L0775: 5, L0777: 5, H0510: 4, L0439: 4, L0747: 4, L0731: 4, L0757: 4, L0601: 4, S0026: 4, H0556: 3, H0509: 3, L0662: 3, L0805: 3, L0776: 3, L0581: 3, L0608: 3, H0624: 2, T0002: 2, S0218: 2, S0354: 2, S0007: 2, H0333: 2, H0574: 2, H0599: 2, L0471: 2, H0373: 2, H0188: 2, H0644: 2, H0040: 2, L0761: 2, L0363: 2, L0766: 2, L0651: 2, L0659: 2, L0783: 2, L0789: 2, H0521: 2, S0028: 2, L0744: 2, L0748: 2, L0745: 2, L0749: 2, L0588: 2, L0362: 2, T0049: 1, H0657: 1, | 18 | |

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| | H0341: 1, H0638: 1, S0444: 1, H0637: 1, H0208: 1, H0441: 1, H0431: 1, H0586: 1, L0623: 1, H0013: 1, S0280: 1, H0575: 1, T0082: 1, H0581: 1, S0049: 1, L0033: 1, H0596: 1, L0040: 1, H0231: 1, S0362: 1, H0355: 1, H0622: 1, T0023: 1, S0366: 1, H0135: 1, H0163: 1, H0591: 1, H0551: 1, T0067: 1, H0059: 1, L0564: 1, S0142: 1, S0344: 1, L0764: 1, L0773: 1, L0768: 1, L0389: 1, L0804: 1, L0376: 1, L0527: 1, L0809: 1, L0665: 1, H0144: 1, H0547: 1, H0519: 1, S0126: 1, H0672: 1, S0330: 1, H0522: 1, H0134: 1, S0037: 1, L0754: 1, L0752: 1, L0755: 1, S0031: 1, H0707: 1, H0667: 1, H0542: 1, H0543: 1 and H0008: 1. |
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| 289 | HTPII72 | 1104236 | 299 | 1 - 570 | 1199 | Pro-21 to Asp-26, Asp-74 to Ser-83, Glu-104 to Asn-110, Gln-161 to Cys-167. | AR061: 10, AR089: 5 H0254: 1, H0255: 1, H0393: 1, H0333: 1, H0486: 1, N0009: 1, H0618: 1, H0622: 1 and H0625: 1. | | |
| | | 958035 | 835 | 1 - 828 | 1735 | Pro-21 to Asp-26, Asp-74 to Ser-83, Glu-104 to Asn-110, Gln-161 to Cys-167, Pro-189 to Pro-195. | | | |
| 290 | H6BSE22 | 1151371 | 300 | 147 - 662 | 1200 | Met-4 to Lys-12, Gln-52 to Pro-72, Cys-80 to Gln-92, Thr-100 to Pro-105, Thr-149 to Asn-158, Leu-161 to Lys-172. | AR089: 1, AR061: 0 H0521: 4, L0766: 3, L0768: 2, S0152: 2, S0028: 2, S0308: 2, L0593: 2, S0212: 1, S0282: 1, H0662: 1, H0305: 1, S0358: 1, H0676: 1, H0580: 1, S0046: 1, H0586: 1, H0492: 1, H0013: 1, H0263: 1, H0046: 1, H0355: 1, H0416: 1, S0003: 1, H0591: 1, H0379: 1, T0042: 1, L0774: 1, L0784: 1, L0776: 1, L0789: 1, L0664: 1, H0701: 1, H0520: 1, H0547: 1, H0689: 1, H0690: 1, | | |

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| 292 | HDPFM16 | 1193042 | 837 | 2 - 472 | 1737 | Ser-444 to Tyr-466, Gln-489 to Cys-497. | H0635: 1, H0505: 1, H0318: 1, H0581: 1, H0050: 1, H0373: 1, S025Q: 1, S0022: 1, H0553: 1, H0124: 1, L0370: 1, H0561: 1, H0593: 1, S0126: 1, H0435: 1, H0518: 1, H0521: 1, H0626: 1, L0748: 1, L0591: 1, H0542: 1, S0424: 1 and H0677: 1. | | |
| | | 864998 | | | | Tyr-21 to Asp-26, Lys-32 to Ala-38, Phe-48 to Glu-57, His-63 to Thr-71. | | | |
| | | 1193042 | 302 | 596 - 1801 | 1202 | Glu-1 to Gly-10, Arg-22 to Lys-27, Pro-99 to Asn-116, Lys-122 to Thr-132, Thr-150 to Asn-159, Ser-187 to Tyr-192, Leu-238 to Cys-252, Glu-272 to Tyr-277, Ile-283 to Met-292, Asp-321 to Ser-328, Lys-365 to Pro-378, Gly-386 to Gln-391. | AR089: 6, AR061: 2 H0457: 3, L0438: 3, L0748: 3, S0214: 2, H0038: 2, L0766: 2, L0731: 2, S0242: 2, H0677: 2, S0134: 1, S0346: 1, H0266: 1, H0644: 1, H0488: 1, S0210: 1, H0529: 1, L0800: 1, L0794: 1, H0521: 1, S0312: 1, L0439: 1, L0749: 1, L0750: 1 and H0423: 1. | | |
| | | 810401 | 838 | 13 - 357 | 1738 | Asp-10 to Lys-18. | | | |

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| 293 | HFPCN10 | 1151478 | 303 | 81 - 548 | 1203 | Ser-26 to Ser-34, Ser-43 to Lys-50. Ala-8 to Ser-23, Ser-68 to Gln-81. | AR061: 97, AR089: 57 H0556: 2, L0745: 2, H0542: 2, H0265: 1, S0222: 1 and L0471: 1. | | | |
| 294 | HLQFO35 | 915568 1161174 | 839 304 | 81 - 551 747 - 1037 | 1739 1204 | Ala-8 to Ser-23, Ser-68 to Gln-81. His-32 to His-38. | AR061: 2, AR089: 1 S0412: 27, L0756: 3, H0644: 2, L0745: 2, H0574: 1, H0032: 1, L0598: 1, L0667: 1, L0766: 1, L0653: 1, L0749: 1, L0779: 1, L0759: 1 and S0026: 1. | | | |
| 295 | HMWU94 | 933901 1150834 | 840 305 | 80 - 184 105 - 572 | 1740 1205 | Lys-75 to Asn-83, Leu-114 to Phe-121, Gln-145 to Lys-156. | AR061: 120, AR089: 64 H0341: 1, H0561: 1, L0790: 1 and L0777: 1. | | | |
| 296 | HSATQ28 | 705880 1124600 | 841 306 | 105 - 443 138 - 491 | 1741 1206 | Pro-1 to Ser-8, Ser-10 to Ile-31, Ser-39 to Asp-48. | AR089: 120, AR061: 12 S0114: 2, H0422: 2 and L0748: 1. | | | |
| 297 | HTPIL46 | 866951 1196787 | 842 307 | 3 - 164 225 - 1898 | 1742 1207 | Ser-14 to Thr-19, Thr-38 to Lys-44. | AR089: 12, AR061: 5 L0748: 14, H0457: 8, L0731: 5, L0770: 4, | | | |

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| | H0521: 4, L0747: 4, H0543: 4, H0486: 3, H0591: 3, H0436: 3, L0777: 3, S0192: 3, H0542: 3, H0422: 3, S0046: 2, S0002: 2, L0667: 2, L0775: 2, L0655: 2, L0439: 2, L0749: 2, L0594: 2, H0170: 1, S0342: 1, S0114: 1, S0134: 1, S0001: 1, H0459: 1, S0222: 1, H0610: 1, H0013: 1, H0635: 1, H0575: 1, H0050: 1, H0271: 1, H0687: 1, S0214: 1, H0622: 1, L0483: 1, H0032: 1, H0038: 1, H0264: 1, H0560: 1, H0641: 1, H0647: 1, L0761: 1, L0771: 1, L0662: 1, L0766: 1, L0803: 1, L0650: 1, L0774: 1, L0805: 1, L0659: 1, L0789: 1, L0790: 1, H0699: 1, H0547: 1, S0152: 1, L0757: 1, H0445: 1, S0308: 1, L0601: 1, S0011: 1 and S0242: 1. |
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| 298 | HNGEN37 | 973570 | 843 | 2 - 2218 | 1743 | Gln-4 to Cys-9, Asp-23 to Pro-35, Leu-54 to Ile-59, Asn-61 to Asp-67, Val-93 to Lys-101, Gly-108 to Glu-136, Ser-145 to Thr-157, Thr-176 to Gln-186, Thr-194 to His-200, Lys-208 to Ser-215, Val-261 to Phe-267, Thr-297 to Arg-305, Lys-320 to Arg-327, Asn-336 to Asn-342, Glu-356 to Glu-365, Lys-375 to Tyr-385, Pro-407 to Val-413, Ser-417 to Leu-423, Thr-459 to Glu-467, Glu-503 to Val-508, Leu-564 to Cys-571, Glu-581 to Asp-590, Pro-611 to Val-621, Lys-625 to Gly-635, Asp-676 to Phe-684, Leu-709 to Cys-717. | AR089: 1, AR061: 0 S0052: 2 | | | |
| | | 1103305 | 308 | 1 - 531 | 1208 | Asn-10 to Arg-15, Asn-22 to Leu-27, Arg-90 to Lys-95. | | | | |
| | | 663955 | 844 | 2 - 259 | 1744 | Asn-9 to Arg-14, | | | | |

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| 299 | HLMDO77 | 974855 | 309 | 32 - 547 | 1209 | Asn-21 to Leu-26. | AR061: 6, AR089: 6, AR051: 3, AR050: 2, AR054: 1 | | | |
| 300 | HNKAZ51 | 974856 | 845 | 403 - 215 | 1745 | Gly-1 to Cys-9, Pro-12 to Pro-36. | | | | |
| | | 1154961 | 310 | 31 - 957 | 1210 | Arg-11 to Arg-18, Gln-96 to Gln-102, Gln-121 to Gln-128, Gly-208 to Gln-216, Pro-231 to Ile-238. | AR050: 2, AR061: 1, AR089: 0, AR054: 0, AR051: 0 L0015: 1 and S0330: 1. | | | |
| | | 947067 | 846 | 31 - 612 | 1746 | Arg-11 to Arg-18, Gln-96 to Gln-102, Gln-121 to Gln-128. | | | | |
| 301 | HOGDR01 | 919899 | 311 | 3 - 977 | 1211 | Cys-49 to Leu-55, Glu-62 to Glu-68, Phe-100 to Lys-106, Pro-122 to Gln-127, Leu-219 to Gly-225, Gly-273 to Gly-281. | AR054: 7, AR089: 2, AR061: 2, AR051: 1, AR050: 0 L0662: 3, L0653: 3, L0648: 2, L0659: 2, L0666: 2, H0435: 2, S0376: 1, H0550: 1, H0264: 1, S0472: 1, L0800: 1, L0643: 1, L0649: 1, L0803: 1, L0790: 1, H0672: 1, S0328: 1, L0779: 1 and S0260: 1. | | | |
| | | 947085 | 847 | 2 - 967 | 1747 | Cys-46 to Leu-52, Glu-59 to Glu-65. | | | | |

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| 302 | HUKEP18 | 957456 | 312 | 852 - 265 | 1212 | | AR061: 14, AR054: 11, AR050: 9, AR089: 4 L0758: 2, H0059: 1, L0789: 1, L0665: 1, L0749: 1 and L0779: 1. | | |
| 303 | HWHGF95 | 1155021 | 313 | 3 - 743 | 1213 | Glu-25 to Trp-33, Trp-76 to Gln-83, Pro-94 to Asp-108. | AR050: 3, AR061: 2, AR054: 2, AR089: 1, AR051: 0 H0586: 1 and L0376: 1. | | |
| | | 947019 | 848 | 2 - 742 | 1748 | Glu-25 to Trp-33, Trp-76 to Gln-83, Pro-94 to Asp-108. | | | |
| 304 | HEMFC61 | 836514 | 314 | 1 - 714 | 1214 | Glu-4 to Ser-9, Ser-58 to Arg-65. | AR061: 4, AR089: 3 H0038: 7, L0758: 5, H0616: 4, L0731: 4, S0002: 3, L0637: 3, H0623: 2, L0794: 2, L0809: 2, L0663: 2, H0522: 2, L0779: 2, L0777: 2, S0046: 1, H0431: 1, T0060: 1, H0013: 1, S0010: 1, H0545: 1, H0050: 1, S0023: 1, S0003: 1, H0328: 1, H0135: 1, H0163: 1, H0412: 1, H0102: 1, H0100: 1, T0042: 1, L0768: 1, | | |

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| | | | | | | | | | L0803: 1, L0375: 1, L0542: 1, L0647: 1, L0367: 1, L0791: 1, L0664: 1, H0693: 1, S0328: 1, S0168: 1, S0031: 1 and H0008: 1. | | | |
| 305 | HEOQP44 | 942596 | 315 | 157 - 1026 | 1215 | Phe-62 to Arg-67, Gln-92 to Leu-104, Arg-163 to Leu-171, Ile-175 to Thr-182, Ser-237 to Ser-244, Ala-270 to Arg-277. | | | AR089: 1, AR061: 0 H0457: 2 | | | |
| 306 | HHEKZ12 | 878267 | 316 | 9 - 395 | 1216 | Phe-62 to Arg-67, Gln-92 to Leu-104. | | | AR089: 1, AR061: 0 H0542: 1 | | | |
| 307 | HHELA35 | 878217 | 317 | 25 - 462 | 1217 | Phe-62 to Arg-67, Gln-92 to Leu-104. | | | AR089: 1, AR061: 0 H0542: 1 | | | |
| 308 | HSYBQ34 | 918789 | 318 | 96 - 1 | 1218 | | | | AR054: 22, AR050: 2, AR051: 1, AR089: 0, AR061: 0 H0624: 2, S0003: 2, H0519: 2, L0591: 2, H0171: 1, H0583: 1, S0418: 1, S0046: 1, H0619: 1, H0437: 1, H0497: 1, H0036: 1, H0590: 1, H0188: 1, H0039: 1, H0551: 1, H0623: 1, H0529: 1, H0520: 1, H0521: 1, H0522: 1, L0745: 1, | | | |

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| 309 | HFCBA44 | 972295 | 849 | 2604 - 3473 | 1749 | | Phe-62 to Arg-67, Gln-92 to Leu-104. | AR089: 14, AR061: 9 H0457: 1, H0009: 1, L0666: 1, S0053: 1 and L0741: 1. | | |
| 310 | HOUBE50 | 948519 | 320 | 1 - 243 | 1220 | | Ser-50 to Ser-66. | AR061: 1, AR089: 0 S0040: 1, S0222: 1, L0471: 1 and L0517: 1. | | |
| 311 | HDPAS16 | 734057 | 321 | 1 - 495 | 1221 | | Glu-38 to His-43, Arg-58 to Thr-68. | AR089: 1, AR061: 0 L0803: 6, H0046: 4, L0666: 3, H0521: 3, L0731: 3, H0331: 2, H0574: 2, L0794: 2, L0774: 2, L0747: 2, H0686: 1, H0341: 1, H0545: 1, H0375: 1, H0687: 1, H0428: 1, L0455: 1, H0316: 1, S0036: 1, S0386: 1, S0002: 1, L0369: 1, L0642: 1, L0662: 1, L0364: 1, L0804: 1, L0776: 1, L0655: 1, L0659: 1, L0809: 1, L0663: 1, L0665: 1, H0670: 1, H0478: 1, L0749: 1, L0756: 1, L0752: 1, L0758: 1 | | |

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| | | | | | | | | | H0343: 1, L0608: 1, L0366: 1, S0192: 1, H0543: 1 and H0423: 1. | | | |
| 312 | HFLAA23 | 960332 | 322 | 2 - 784 | 1222 | | | | AR061: 106, AR089: 12 H0047: 2, H0181: 2 and S0260: 1. | | | |
| 313 | HCFMZ90 | 922112 | 323 | 273 - 881 | 1223 | | | Asp-1 to Arg-8, Lys-15 to Asn-20, Thr-74 to Leu-80, Pro-84 to Asp-90. | AR061: 2, AR089: 1 L0749: 1, L0731: 1, L0757: 1 and H0423: 1. | | | |
| 314 | HFCES27 | 1103330 | 324 | 491 - 1120 | 1224 | | | Thr-7 to Leu-13, Pro-17 to Asp-23, Ala-180 to Arg-188. | AR061: 1, AR089: 1 S0045: 2, L0646: 2, L0766: 2, L0776: 2, L0783: 2, L0731: 2, H0341: 1, H0663: 1, T0039: 1, L0021: 1, H0009: 1, T0042: 1, L0763: 1, L0764: 1, L0649: 1, L0775: 1, L0661: 1, S0328: 1, L0777: 1, L0757: 1, L0758: 1 and H0444: 1. | | | |
| 315 | HSDFK78 | 922115 | 850 | 372 - 1001 | 1750 | | | Thr-7 to Leu-13, Pro-17 to Asp-23, Ala-180 to Arg-188. | | | | |
| | | 1155464 | 325 | 1 - 306 | 1225 | | | Tyr-5 to Thr-14, His-61 to Asn-70. | AR089: 6, AR061: 4 H0266: 1, H0416: 1 and S0031: 1. | | | |
| | | 582754 | 851 | 3 - 374 | 1751 | | | Tyr-6 to Thr-13, | | | | |

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| 316 | HSDJX58 | 891067 | 326 | 729 - 1487 | 1226 | His-60 to Asn-69. Tyr-101 to Glu-108, Pro-110 to Arg-116, Tyr-158 to Gln-164. | AR054: 11, AR050: 3, AR051: 3, AR089: 2, AR061: 2 L0748: 7, H0171: 2, H0624: 1, H0341: 1, S0280: 1, H0271: 1, H0032: 1, L0367: 1, L0439: 1, S0031: 1 and S0260: 1. | | |
| 317 | HSLHV27 | 956591 | 852 | 786 - 7 | 1752 | Tyr-101 to Glu-108, Pro-110 to Arg-116, Tyr-158 to Gln-164. His-8 to Gly-18. | AR050: 5, AR061: 2, AR054: 1, AR089: 1 S0028: 1 | | |
| 318 | HNGFU12 | 964075 | 853 | 983 - 21 | 1753 | His-8 to Gly-18. | AR089: 4, AR061: 1 S0052: 1 and S0428: 1. | | |
| 319 | HWLKA89 | 1105515 | 854 | 45 - 290 | 1754 | Leu-59 to Gln-64. | AR089: 2, AR061: 0 S0358: 1, S0370: 1, L0803: 1, S0374: 1 and S0152: 1. | | |
| 320 | HLWBU48 | 735158 | 855 | 1 - 318 | 1755 | Lys-1 to Ile-6, Pro-28 to Glu-37, Leu-58 to Arg-65, Pro-95 to Glu-102, Arg-104 to Gly-111, | AR089: 8, AR061: 5 L0754: 3, H0553: 2, L0731: 2, L0005: 1, H0581: 1, H0271: 1, H0644: 1 and H0521: 1. | | |

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| 321 | HWWEY71 | 1204720 | 721520 | 856 | 2 - 280 | 1756 | <p>Glu-118 to Glu-123, Glu-125 to Ala-130, Gly-142 to Gly-151.</p> <p>Ile-5 to Pro-10, Lys-36 to Thr-41.</p> <p>Pro-17 to His-24, Pro-26 to Asp-33, Pro-66 to Lys-72, Thr-149 to Arg-158, Asp-172 to Glu-178, Ala-279 to Ser-289, Arg-306 to Arg-314, Val-330 to Lys-336, Asp-347 to Arg-353, Arg-358 to Gln-363.</p> | <p>AR089: 1, AR061: 0 H0556: 24, H0521: 12, H0551: 9, H0265: 8, H0692: 8, H0543: 8, S0418: 7, L0748: 7, H0542: 7, H0318: 6, H0560: 6, S0314: 6, H0445: 6, L0665: 5, L0747: 5, H0423: 5, H0341: 4, H0617: 4, L0769: 4, L0439: 4, L0740: 4, L0750: 4, L0595: 4, S0278: 3, H0052: 3, H0622: 3, H0135: 3, H0040: 3, S0144: 3, L0768: 3, L0766: 3, L0775: 3, L0776: 3, H0547: 3, S0328: 3, S0206: 3, L0591: 3, L0608: 3, H0422: 3, H0170: 2, H0657: 2, H0484: 2, S0045: 2, S0046: 2, H0545: 2, H0050: 2, H0012: 2, H0620: 2.</p> | | |
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H0083: 2, H0284: 2, H0087: 2, H0488: 2, L0640: 2, L0771: 2, L0773: 2, L0521: 2, L0363: 2, L0783: 2, L0383: 2, L0663: 2, L0438: 2, H0520: 2, L0751: 2, L0731: 2, L0757: 2, L0596: 2, L0362: 2, T0002: 1, H0686: 1, S0040: 1, S0218: 1, H0583: 1, H0656: 1, S0180: 1, S0212: 1, H0483: 1, H0177: 1, H0125: 1, S0420: 1, S0356: 1, S0376: 1, S0360: 1, S0408: 1, H0208: 1, S0132: 1, H0619: 1, H0393: 1, L0717: 1, H0586: 1, H0587: 1, H0642: 1, H0331: 1, H0256: 1, T0109: 1, H0013: 1, H0599: 1, T0082: 1, S0182: 1, H0309: 1, T0110: 1, H0327: 1, H0544: 1, H0041: 1, S0051: 1, H0266: 1, H0290: 1, H0252: 1, H0328: 1, H0604: 1, H0031: 1,

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| | H0644: 1, H0628: 1, H0181: 1, H0606: 1, S0364: 1, H0068: 1, H0090: 1, H0616: 1, H0264: 1, H0412: 1, H0059: 1, S0038: 1, H0100: 1, L0351: 1, T0042: 1, H0494: 1, H0561: 1, L0065: 1, S0438: 1, H0509: 1, S0150: 1, S0472: 1, H0647: 1, S0422: 1, S0002: 1, S0426: 1, L0500: 1, L0637: 1, L0772: 1, L0372: 1, L0645: 1, L0662: 1, L0364: 1, L0388: 1, L0774: 1, L0375: 1, L0805: 1, L0653: 1, L0655: 1, L0657: 1, L0559: 1, L0659: 1, L0526: 1, L0382: 1, L0792: 1, L0666: 1, L0664: 1, H0144: 1, H0698: 1, H0699: 1, H0703: 1, H0435: 1, S0380: 1, H0522: 1, H0696: 1, S0028: 1, L0744: 1, L0754: 1, L0779: 1, L0758: 1, L0759: 1, L0593: 1 |
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| | | | | | | | | | L0601: 1, S0011: 1, H0668: 1, S0192: 1, S0276: 1 and S0424: 1. | | |
| 322 | HHFGD45 | 970546 | 857 | 71 - 775 | 1757 | Ala-46 to Pro-68, Gln-75 to Gly-84, Leu-106 to Gly-121, Pro-208 to Lys-214. | | | AR061: 2, AR089: 1 S0053: 2, S0045: 1, H0619: 1, H0318: 1 and H0050: 1. | | |
| 323 | HNHEB44 | 584855 1161293 | 858 333 | 1 - 267 643 - 2 | 1758 1233 | Phe-3 to Cys-8, Ser-64 to Gln-69. | | | AR061: 1, AR089: 0 S0053: 2, S0045: 1, H0619: 1, H0318: 1 and H0050: 1. | | |
| 324 | HMACX92 | 683284 1151497 | 859 334 | 1 - 195 119 - 1138 | 1759 1234 | His-27 to Thr-32. Glu-140 to Trp-147, Asn-323 to Glu-329. | | | AR061: 5, AR089: 2 S0144: 4, L0803: 2, H0682: 2, H0521: 2, H0295: 1, L0005: 1, H0645: 1, H0549: 1, T0060: 1, H0327: 1, H0545: 1, H0050: 1, H0012: 1, H0620: 1, H0510: 1, H0687: 1, H0617: 1, H0059: 1, H0509: 1, H0641: 1, S0002: 1, L0646: 1, L0374: 1, L0794: 1, | | |

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| 325 | HNTBW57 | 922250 1193070 | 860 335 | 140 - 1159 1 - 1263 | 1760 1235 | Pro-1 to Gly-18, Arg-29 to Pro-42, Glu-80 to Arg-86, Gly-239 to Pro-247, Pro-410 to Thr-419. | AR089: 0, AR061: 0 L0794: 4, H0435: 2, H0632: 1, H0013: 1, H0030: 1, S0150: 1, L0649: 1, H0547: 1, H0519: 1, H0689: 1, L0759: 1 and H0677: 1. | L0804: 1, L0775: 1, L0656: 1, L0809: 1, L0790: 1, L0664: 1, S0052: 1, H0520: 1, L0749: 1, H0653: 1 and S0194: 1. | |
| 326 | HBSDC13 | 867327 1105677 | 861 336 | 2 - 682 486 - 94 | 1761 1236 | | AR089: 8, AR061: 4 H0305: 4, H0419: 1 and S0045: 1. | | |
| 327 | HCWBX21 | 657402 920486 | 862 337 | 3 - 233 49 - 333 | 1762 1237 | Glu-52 to Gly-57, Cys-69 to Asp-83, Lys-88 to Met-93. | AR061: 1, AR089: 0 H0305: 4, H0419: 1 and S0045: 1. | | |
| 328 | HFRBW72 | 916944 | 338 | 365 - 679 | 1238 | Arg-10 to Lys-16. | AR061: 3, AR089: 1 S0028: 5, S0126: 2, S0001: 1, S0282: 1, S0045: 1, S0049: 1, S0050: 1, H0271: 1, H0388: 1, S0390: 1, S0260: 1 and H0008: 1. | | |
| 329 | HSLJX23 | 1105530 | 339 | 2 - 496 | 1239 | Met-12 to Gly-17. | AR089: 1, AR061: 0 | | |

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| 330 | HSLJX90 | 837470 1105297 | 863 340 | 2 - 256 1 - 438 | 1763 1240 | Glu-29 to Asp-35, Glu-113 to Leu-120, Ala-123 to Gly-133, Ala-138 to Lys-143. Arg-21 to Glu-27. | S0390: 1 and S0031: 1. AR089: 1, AR061: 0 H0150: 1, S0390: 1 and S0027: 1. | | |
| 331 | HAUAI67 | 787575 1102604 | 864 341 | 2 - 358 107 - 727 | 1764 1241 | Arg-13 to Arg-19, Asp-37 to Asp-43, Glu-127 to Asp-132, Asn-152 to Glu-171, Ala-179 to Ala-193. | AR061: 4, AR089: 2 L0748: 18, L0749: 8, L0755: 7, H0686: 4, S0360: 3, H0519: 3, H0659: 3, L0747: 3, L0758: 3, H0341: 2, H0622: 2, H0040: 2, H0616: 2, L0772: 2, L0375: 2, L0754: 2, L0779: 2, H0542: 2, H0294: 1, H0657: 1, H0656: 1, S0116: 1, H0663: 1, H0638: 1, S0376: 1, H0393: 1, H0083: 1, H0030: 1, L0055: 1, H0068: 1, H0591: 1, H0038: 1, H0412: 1, H0100: 1, L0475: 1, S0422: 1, L0763: 1, L0771: 1, L0767: 1, L0768: 1, L0784: 1, L0776: 1, L0633: 1, L0783: 1, | | |

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| 332 | HDPTA89 | 929241 953718 | 865 342 | 230 - 652 20 - 433 | 1765 1242 | Gly-22 to Phe-27, Tyr-36 to Ala-48, Glu-51 to Pro-79, Pro-102 to His-113. | AR089: 1, AR061: 1 L0777: 13, L0751: 10, L0769: 7, L0766: 6, L0758: 6, H0618: 4, H0617: 4, L0771: 4, L0776: 4, L0757: 4, L0759: 4, H0494: 3, L0761: 3, H0521: 3, L0754: 3, H0265: 2, H0650: 2, S0045: 2, H0427: 2, H0253: 2, H0318: 2, H0150: 2, L0794: 2, L0805: 2, L0665: 2, L0743: 2, L0439: 2, L0749: 2, L0750: 2, L0752: 2, H0445: 2, H0556: 1, S0342: 1, S0218: 1, L0785: 1, H0484: 1, L0481: 1, S0418: 1, S0420: 1, H0637: 1, H0549: 1, H0587: 1, H0333: 1, H0486: 1. | L0665: 1, H0144: 1, H0682: 1, S0378: 1, H0627: 1, L0752: 1, L0731: 1, S0026: 1, H0665: 1, S0242: 1 and H0543: 1. | | |
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| 333 | HMCBN45 | 927125 | 343 | 3 - 686 | 1243 | Lys-50 to Gly-56, Pro-114 to Gly-122, Glu-129 to Tyr-134, Ala-174 to Leu-179, Arg-210 to Tyr-222. | S0280: 1, H0599: 1, S0346: 1, H0194: 1, T0115: 1, H0597: 1, H0231: 1, H0046: 1, H0083: 1, H0266: 1, H0188: 1, H0688: 1, H0424: 1, H0213: 1, H0181: 1, S0364: 1, H0616: 1, H0087: 1, H0551: 1, H0412: 1, H0623: 1, H0100: 1, T0041: 1, S0150: 1, H0695: 1, L0796: 1, L0643: 1, L0662: 1, L0803: 1, L0775: 1, L0809: 1, L0789: 1, L0663: 1, L0664: 1, H0691: 1, S0126: 1, H0682: 1, S0152: 1, H0555: 1, H0627: 1, S0027: 1, L0779: 1, L0780: 1, L0753: 1, L0596: 1, H0668: 1, H0667: 1 and H0543: 1. | AR089: 9, AR061: 8 T0042: 2, H0556: 1, H0486: 1, L0586: 1, H0083: 1, H0641: 1, S0142: 1, H0529: 1 and H0435: 1 |
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| 334 | HTTJY18 | 1223495 | 344 | 352 - 1281 | 1244 | Ala-7 to His-20, Arg-38 to Gly-48, His-89 to Trp-98, Thr-125 to Arg-130, Ala-133 to Cys-140, Ser-157 to Leu-171, Asp-201 to Ile-206, Gln-231 to Lys-238, Thr-240 to Thr-259, Gly-266 to Gly-277. | AR089: 1, AR061: 0 L0766: 50, L0754: 12, L0740: 11, S0358: 9, L0803: 8, H0575: 7, L0731: 7, L0747: 6, L0761: 5, L0662: 5, L0805: 5, L0744: 5, L0748: 5, L0779: 5, L0794: 4, L0749: 4, L0750: 4, L0752: 4, L0757: 4, L0362: 4, L0471: 3, S0210: 3, L0806: 3, H0144: 3, S0126: 3, S0328: 3, L0743: 3, L0777: 3, L0759: 3, H0423: 3, S0376: 2, H0013: 2, S0474: 2, H0581: 2, H0179: 2, H0628: 2, H0038: 2, H0264: 2, H0623: 2, H0641: 2, S0142: 2, S0426: 2, L0800: 2, L0771: 2, L0768: 2, L0649: 2, L0774: 2, L0655: 2, L0607: 2, L0791: 2, S0374: 2, L0438: 2, H0436: 2, L0745: 2, L0746: 2, L0756: 2, L0753: 2, L0755: 2, S0026: 2, H0170: 1, | | |
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| | S0114: 1, H0341: 1, S0001: 1, H0664: 1, H0638: 1, S0442: 1, S0046: 1, S6022: 1, H0611: 1, H0370: 1, H0642: 1, L0021: 1, H0599: 1, H0003: 1, L0022: 1, H0036: 1, H0004: 1, H0274: 1, S0010: 1, L0105: 1, H0421: 1, H0052: 1, H0251: 1, H0596: 1, H0046: 1, H0572: 1, H0050: 1, H0242: 1, H0012: 1, S0050: 1, H0014: 1, H0083: 1, H0375: 1, S0250: 1, S0003: 1, T0023: 1, L0483: 1, T0006: 1, H0031: 1, L0142: 1, L0055: 1, H0032: 1, H0674: 1, L0455: 1, S0036: 1, H0135: 1, H0090: 1, H0040: 1, H0634: 1, H0616: 1, T0067: 1, H0488: 1, H0433: 1, H0413: 1, H0056: 1, H0560: 1, L0598: 1, H0529: 1, L0369: 1, L0762: 1, L0770: 1, L0638: 1, | |
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| | | | | | | | | | L0373: 1, L0372: 1, L0764: 1, L0773: 1, L0804: 1, L0776: 1, L0659: 1, L0518: 1, L0384: 1, L0789: 1, L0790: 1, L0666: 1, L0663: 1, L0664: 1, S0148: 1, H0547: 1, H0659: 1, H0670: 1, H0539: 1, S0378: 1, H0518: 1, H0521: 1, H0696: 1, H0555: 1, H0478: 1, S0028: 1, L0758: 1, H0445: 1, L0588: 1, S0192: 1, H0543: 1, S0458: 1 and S0384: 1. | | |
| 335 | HMAJL09 | 950989 | 866 | 238 - 1263 | 1766 | Asp-1 to Pro-17. | AR089: 0, AR061: 0 S0278: 1 | | | | |
| | | 1157337 | 345 | 68 - 526 | 1245 | Tyr-22 to Arg-30, Arg-77 to Gly-83. | | | | | |
| | | 950168 | 867 | 2 - 493 | 1767 | Tyr-30 to Ser-35, Arg-94 to Gly-100. | | | | | |
| 336 | HSVCH37 | 558195 | 346 | 3 - 122 | 1246 | | AR089: 1, AR061: 1 H0309: 2 | 4q25-q27 | 137600, 147680, 189800, 217030, 248510, 600919, 601542 | | |
| 337 | HTOCG37 | 708888 | 347 | 3 - 218 | 1247 | Asn-7 to Thr-18. | AR061: 11, AR089: 6 | | | | |

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| 338 | HBXAW47 | 771624 | 348 | 243 - 656 | 1248 | His-8 to Arg-13, Ser-23 to Lys-30. | Glu-34 to Ser-39, His-59 to Asn-64. | L0777: 4, L0766: 3, L0776: 3, L0439: 3, H0031: 2, L0809: 2, H0694: 2, L0591: 2, S6024: 1, H0656: 1, H0369: 1, H0051: 1, T0067: 1, H0272: 1, L0769: 1, L0805: 1, L0518: 1, L0519: 1, H0684: 1, L0779: 1, S0031: 1, L0584: 1 and L0366: 1. | | |
| | | | | | | | | AR089: 5, AR061: 1 L0748: 5, L0438: 3, L0747: 3, L0731: 3, L0005: 2, S0360: 2, L0769: 2, L0794: 2, L0766: 2, L0803: 2, L0655: 2, L0756: 2, L0758: 2, S0356: 1, L0717: 1, H0033: 1, H0617: 1, H0413: 1, S0038: 1, S0422: 1, S0426: 1, L0639: 1, L0646: 1, L0662: 1, L0378: 1, L0636: 1, L0647: 1, L0367: 1, L0789: 1, L0666: 1, H0436: 1, L0779: 1, L0777: 1, L0752: 1. | | |

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| 339 | HBXAW27 | 909801 | 349 | 1111 - 1830 | 1249 | Gly-19 to Cys-25, Pro-56 to Phe-68, Gly-94 to Pro-99, Lys-113 to Leu-119, Pro-126 to Gln-131, Lys-138 to Leu-145. | L0753: 1, L0608: 1 and L0601: 1. AR089: 2, AR061: 1 L0741: 10, H0052: 6, S0036: 3, L0439: 3, S0388: 2, L0770: 2, L0438: 2, S0300: 1, S0222: 1, H0441: 1, L0021: 1, S0010: 1, S0049: 1, H0327: 1, H0150: 1, H0009: 1, H0569: 1, H0051: 1, S0051: 1, T0010: 1, L0456: 1, S0038: 1, H0100: 1, L0370: 1, L0517: 1, L0742: 1, L0745: 1, L0592: 1 and L0366: 1. | 12q13 | 107777, 123940, 139350, 139350, 148040, 148041, 148043, 148070, 231550, 600194, 600231, 600536, 600808, 600956, 601284, 601769, 601769, 601928, 602116, 602153 |
| 340 | HSLJE54 | 926924 | 350 | 3 - 731 | 1250 | Arg-1 to Gly-7, Pro-25 to His-34, Leu-36 to Lys-49. | AR061: 0, AR089: 0 S0036: 1, H0521: 1, H0436: 1 and S0390: 1. | | |
| 341 | HBXBG65 | 932780 | 351 | 2 - 535 | 1251 | Asn-1 to Arg-10, Pro-105 to Val-114, Gln-130 to Glu-140. | AR089: 1, AR061: 0 H0144: 2, S0038: 1 and L0439: 1. | 14q32.1. | 107280, 107280, 107400, 107400, 122500, |

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| | | | | | | | | | 186960, 245200, 601841 |
| 342 | HE8CG83 | 933609 | 352 | 703 - 1128 | 1252 | | | AR089: 17, AR061: 8 L0748: 3, H0650: 1, S0007: 1, H0013: 1, H0618: 1, H0051: 1, S0051: 1, H0553: 1, H0268: 1 and S0031: 1. | |
| 343 | HOGCW55 | 953161 | 353 | 90 - 392 | 1253 | | | AR061: 1, AR089: 1 H0620: 3 and H0435: 1. | |
| 344 | HNTND64 | 954871 | 354 | 1 - 264 | 1254 | Gln-34 to Glu-42. | | AR089: 8, AR061: 5 S0040: 1, H0083: 1 and H0520: 1. | |
| 345 | HHAWC08 | 957942 | 355 | 172 - 1047 | 1255 | Pro-14 to Gly-32, Pro-73 to Glu-83, Phe-92 to Ser-100, Glu-141 to Asp-148, Thr-159 to Gln-166, Asp-198 to Pro-204, Thr-242 to Val-248. | | AR061: 0, AR089: 0 H0052: 2, L0439: 2, S0418: 1, H0619: 1, S0280: 1 and L0438: 1. | |
| 346 | HFPEN04 | 964824 | 356 | 88 - 540 | 1256 | Glu-62 to Tyr-67, Ser-129 to Asp-135. | | AR061: 5, AR089: 2 S0010: 4, S0222: 3, H0455: 2, L0803: 2, L0439: 2, L0745: 2, S0282: 1, S0400: 1, H0456: 1, H0441: 1, S0346: 1, H0509: 1, L0769: 1, L0438: 1, | |

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| 347 | HTZMB51 | 496523 | 357 | 58 - 399 | 1257 | Cys-1 to Asp-10, Thr-16 to Asn-22. | L0756: 1 and S0106: 1. AR089: 1, AR061: 1 S0045: 1, H0623: 1 and S3020: 1. | | |
| 348 | HNHDK43 | 529500 | 358 | 1 - 396 | 1258 | Thr-7 to Gly-13. | S0053: 1 and S0037: 1. | | |
| 349 | HTTDP32 | 558751 | 359 | 1 - 360 | 1259 | Asn-21 to Asn-31. | AR061: 4, AR089: 3 L0789: 2, H0069: 1, H0052: 1, H0266: 1, H0040: 1, S0210: 1 and H0519: 1. | 116806, 120120, 120120, 120120, 120120, 120436, 120436, 120436, 138320, 168468, 182280, 190182, 190182, 227646, 261510, 600163, 601154 | |
| 350 | HSLFP27 | 572920 | 360 | 478 - 2 | 1260 | Phe-44 to Arg-49. | AR089: 1, AR061: 0 S0126: 4, S0028: 2 and S0031: 2. | | |
| 351 | HMTAL73 | 621705 | 361 | 73 - 450 | 1261 | Val-99 to Gly-106. | AR089: 2, AR061: 2 H0518: 1 and L0362: 1. | 192340, 234200 | |
| 352 | HMHQBQ53 | 715301 | 362 | 404 - 201 | 1262 | Asp-22 to Gly-34, Lys-37 to Glu-42. | AR089: 39, AR061: 13 L0745: 8, L0740: 6, L0747: 5, L0794: 4, | | |

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| | L0666: 4, S0360: 3, H0150: 3, H0031: 3, H0617: 3, L0769: 3, H0662: 2, S0182: 2, H0286: 2, H0135: 2, L0770: 2, L0662: 2, L0803: 2, H0547: 2, L0743: 2, L0752: 2, L0753: 2, L0731: 2, L0758: 2, L0593: 2, H0556: 1, S0342: 1, H0341: 1, S0212: 1, H0671: 1, S0418: 1, S0420: 1, S0358: 1, H0392: 1, H0587: 1, H0575: 1, H0253: 1, H0318: 1, H0052: 1, H0545: 1, H0046: 1, H0050: 1, H0408: 1, H0510: 1, H0375: 1, H0099: 1, H0247: 1, H0687: 1, H0628: 1, H0551: 1, H0509: 1, S0344: 1, S0210: 1, L0761: 1, L0772: 1, L0646: 1, L0643: 1, L0764: 1, L0364: 1, L0774: 1, L0653: 1, L0655: 1, L0636: 1, L0783: 1, L0809: 1, H0144: 1, L0438: 1, | |
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| 353 | HBICG44 | 715860 | 363 | 377 - 138 | 1263 | | H0593: 1, S0330: 1, H0518: 1, L0748: 1, L0439: 1, L0751: 1, L0754: 1, L0749: 1, L0757: 1, L0759: 1, H0653: 1, H0542: 1 and H0423: 1. | AR061: 22, AR089: 5 18 L0803: 23, S0360: 7, S0358: 6, L0794: 5, L0777: 5, H0510: 4, L0439: 4, L0731: 4, L0757: 4, S0026: 4, H0509: 3, L0662: 3, L0805: 3, L0608: 3, H0624: 2, T0002: 2, S0218: 2, S0007: 2, H0333: 2, H0574: 2, L0471: 2, H0373: 2, H0188: 2, H0644: 2, L0363: 2, L0766: 2, L0774: 2, L0651: 2, L0776: 2, L0659: 2, L0789: 2, H0521: 2, L0748: 2, L0745: 2, L0747: 2, L0749: 2, L0581: 2, L0362: 2, L0601: 2, H0556: 1, T0049: 1, H0657: 1, H0638: 1 S0354: 1 | | |
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| 354 | HSKXN70 | 753717 | 364 | 3 - 356 | 1264 | Glu-30 to Glu-38, Asn-47 to Tyr-58. | AR089: 1, AR061: 1 L0439: 4, L0770: 2, L0794: 2, L0438: 2, L0740: 2, H0599: 1, T0082: 1, S0003: 1, H0644: 1, L0639: 1 | S0444: 1, H0637: 1, H0208: 1, H0441: 1, H0431: 1, H0586: 1, L0623: 1, S0280: 1, H0575: 1, T0082: 1, H0581: 1, S0049: 1, L0033: 1, H0596: 1, L0040: 1, H0231: 1, H0355: 1, H0622: 1, T0023: 1, S0366: 1, H0163: 1, H0040: 1, H0551: 1, T0067: 1, L0564: 1, L0764: 1, L0389: 1, L0804: 1, L0775: 1, L0376: 1, L0527: 1, L0783: 1, L0809: 1, L0665: 1, H0144: 1, H0672: 1, S0330: 1, H0522: 1, H0134: 1, S0028: 1, L0744: 1, L0754: 1, L0755: 1, S0031: 1, L0588: 1, H0543: 1 and H0008: 1. | |
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| 355 | HP\AC32 | 815942 | 365 | 3 - 371 | 1265 | | | AR089: 1, AR061: 0 S0028: 2, H0624: 1, S0278: 1, S0150: 1 and H0689: 1. | | | |
| 356 | HHFFP57 | 835955 | 366 | 128 - 688 | 1266 | | | AR061: 4, AR089: 4 | | | |
| 357 | HFKJW01 | 836491 | 367 | 3 - 440 | 1267 | | | AR089: 1, AR061: 0 H0620: 2, H0012: 1, S0152: 1 and S0260: 1. | | | |
| 358 | HSDFL63 | 836498 | 368 | 1 - 249 | 1268 | | Glu-1 to Asp-7, Met-53 to Met-60, Phe-78 to Ser-83. | AR061: 402, AR089: 142 H0038: 7, L0758: 5, H0616: 4, L0731: 4, S0002: 3, L0637: 3, H0623: 2, L0794: 2, L0809: 2, L0663: 2, H0522: 2, L0779: 2, L0777: 2, S0046: 1, H0431: 1, T0060: 1, H0013: 1, S0010: 1, H0545: 1, H0050: 1, S0023: 1, S0003: 1, H0328: 1, H0135: 1, H0163: 1, H0412: 1, H0102: 1, H0100: 1, T0042: 1, L0768: 1, L0803: 1, L0375: 1, | | | |

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| | | | | | | | | | L0542: 1, L0647: 1, L0367: 1, L0791: 1, L0664: 1, H0693: 1, S0328: 1, S0168: 1, S0031: 1 and H0008: 1. | | |
| 359 | HLD0008 | 857070 | 369 | 3 - 449 | 1269 | Phe-13 to Lys-19, Gln-21 to Ser-37, Arg-44 to Tyr-60, Cys-84 to Asn-89, Thr-122 to Thr-128. | | | AR089: 3, AR061: 3 H0333: 1 and H0510: 1. | | |
| 360 | HMSHN43 | 867363 | 370 | 49 - 375 | 1270 | Pro-16 to Arg-23. | | | AR061: 7, AR089: 4 S0354: 2, S0212: 1, H0484: 1, H0402: 1, S0358: 1, H0457: 1, H0213: 1, H0634: 1, H0059: 1, H0494: 1, S0002: 1, L0648: 1, L0438: 1, H0521: 1 and L0751: 1. | | |
| 361 | HBXCT92 | 871044 | 371 | 3 - 1451 | 1271 | Pro-18 to Trp-25, Arg-164 to Ser-169, Pro-174 to Gln-185, Lys-220 to Phe-226, Ser-272 to Lys-290, Cys-316 to Val-329, Glu-431 to Gln-436, Ile-463 to Val-470. | | | AR089: 1, AR061: 1 H0544: 4, L0438: 4, L0439: 3, L0747: 3, S0036: 2, L0794: 2, H0539: 2, L0748: 2, L0485: 2, S0424: 2, S0116: 1, S0360: 1, S0046: 1, H0411: 1, H0261: 1, H0455: 1, H0574: 1, H0632: 1, L0021: 1, H0575: 1, | | |

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| 362 | H6EDP44 | 875744 | 372 | 157 - 876 | 1272 | | | | H0618: 1, H0052: 1, H0251: 1, H0309: 1, H0327: 1, S0050: 1, S6028: 1, L0456: 1, S0038: 1, H0494: 1, L0520: 1, L0764: 1, L0375: 1, L0657: 1, L0528: 1, H0660: 1, S0044: 1, S0028: 1, L0758: 1, L0759: 1, L0596: 1, L0592: 1, S0011: 1 and S0192: 1. | | |
| 363 | HLJBF94 | 875745 | 373 | 153 - 668 | 1273 | Arg-1 to Trp-9, Ala-25 to Ser-30. | | | AR061: 6, AR089: 2 | | |
| | | | | | | | | | AR089: 4, AR061: 4 H0265: 3, H0592: 2, H0494: 2, L0761: 2, L0374: 2, L0804: 2, H0519: 2, H0593: 2, H0556: 1, H0657: 1, H0656: 1, H0662: 1, S0358: 1, S0376: 1, H0437: 1, H0253: 1, H0375: 1, H0059: 1, L0646: 1, L0768: 1, L0766: 1, L0803: 1, L0774: 1, L0775: 1, L0658: 1, L0809: 1, L0666: 1, H0520: 1, H0539: 1 S0027: 1 and | | |

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| 364 | HTEHO28 | 877182 | 374 | 1286 - 438 | 1274 | Ser-14 to Gln-19. | H0543: 1. AR061: 7, AR089: 4 T0039: 1, H0123: 1, H0038: 1, H0040: 1, T0042: 1, S0126: 1, H0631: 1, L0596: 1 and H0506: 1. | | |
| 365 | HE9PC30 | 880696 | 375 | 1 - 390 | 1275 | Arg-2 to Lys-28, Lys-43 to His-48, Arg-66 to Gly-76, His-117 to Cys-130. | AR089: 2, AR061: 2 L0766: 17, H0038: 2, L0794: 2, L0803: 2, H0144: 2, L0362: 2, S0114: 1, H0013: 1, H0575: 1, H0596: 1, H0046: 1, L0471: 1, S0250: 1, L0142: 1, H0628: 1, H0032: 1, H0135: 1, H0634: 1, H0616: 1, H0413: 1, H0056: 1, S0142: 1, L0598: 1, L0774: 1, L0789: 1, L0790: 1, L0791: 1, S0126: 1, H0478: 1, S0028: 1, L0743: 1, L0744: 1, L0754: 1, L0745: 1, L0746: 1, L0747: 1, L0750: 1, L0752: 1, L0731: 1 and L0757: 1. | | |
| 366 | HLMDN29 | 881288 | 376 | 3 - 509 | 1276 | Glu-15 to Glu-26, Thr-60 to Ile-66, | AR061: 5, AR089: 2 H0254: 1, H0255: 1, | | |

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| 367 | HWBCF78 | 911355 | 377 | 1 - 330 | 1277 | Gly-82 to Tyr-88. Pro-1 to Gly-9, Pro-11 to Gly-18, Asp-35 to Arg-55. | H0705: 1 and H0412: 1. AR089: 1, AR061: 1 H0457: 12, H0521: 11, H0179: 6, H0402: 5, H0271: 3, H0581: 2, H0188: 2, S0002: 2, S0053: 2, H0522: 2, H0436: 2, H0254: 1, H0255: 1, H0306: 1, H0638: 1, H0637: 1, H0580: 1, H0619: 1, S0278: 1, H0587: 1, H0486: 1, S0049: 1, H0050: 1, H0510: 1, H0252: 1, H0553: 1, H0606: 1, S0142: 1, S0344: 1, H0529: 1, L0763: 1, L0770: 1, L0667: 1, L0767: 1, L0794: 1, L0774: 1, L0653: 1, L0659: 1, L0788: 1, S0052: 1, S0330: 1, H0555: 1, S0308: 1, L0592: 1, H0667: 1 and S0424: 1. | | |
| 368 | HUKEN49 | 911465 | 378 | 92 - 340 | 1278 | Pro-11 to Glu-17. | AR061: 1, AR089: 1 L0758: 19, L0777: 16, L0750: 14, L0747: 13, L0748: 10, H0692: 9, L0775: 6, L0749: 6, | | |

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| 369 | HCUDS02 | 914401 | 379 | 63 - 860 | 1279 | Pro-16 to Arg-23, Thr-148 to Leu-155, Phe-203 to Asp-214, Pro-255 to Ser-265. | AR089: 13, AR061: 6 S0354: 2, S0212: 1, H0484: 1, H0402: 1, S0358: 1, H0059: 1, H0494: 1, S0002: 1, L0438: 1, H0521: 1 and | | | | | | |

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| 370 | HTTJU40 | 914402 | 380 | 16 - 495 | 1280 | Thr-71 to Leu-78, Phe-126 to Gly-133, Arg-150 to Gly-159. | L0751: 1. AR089: 1, AR061: 1 H0457: 1, H0213: 1, H0634: 1 and S0002: 1. | | |
| 371 | HFXJX41 | 915649 | 381 | 296 - 682 | 1281 | Arg-1 to Lys-10, Gln-39 to Asp-44. | AR061: 0, AR089: 0 S0282: 1, S0150: 1 and S0260: 1. | | |
| 372 | HSLCK91 | 915650 | 382 | 1 - 399 | 1282 | | AR089: 1, AR061: 0 S0028: 2, S0142: 1 and S0344: 1. | | |
| 373 | HSLAO29 | 917349 | 383 | 3 - 452 | 1283 | Ala-40 to Leu-47, Gln-79 to Cys-84, Cys-95 to Thr-100. | AR061: 17, AR089: 4 H0556: 18, H0265: 8, H0692: 8, L0748: 7, H0543: 7, S0418: 6, L0665: 5, L0747: 5, H0445: 5, H0542: 5, H0318: 4, H0617: 4, L0769: 4, H0521: 4, L0750: 4, H0423: 4, H0135: 3, H0551: 3, H0560: 3, L0768: 3, L0766: 3, L0775: 3, L0776: 3, S0328: 3, S0314: 3, S0206: 3, L0439: 3, L0740: 3, L0591: 3, L0608: 3, H0170: 2, H0657: 2, H0484: 2, H0052: 2, H0545: 2, H0012: 2, H0620: 2, H0083: 2, | 12q12-q14 | 123829, 147570, 181430, 252940, 264700, 600194, 600231, 600808, 601284, 601769, 601769, 602116 |

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| 375 | HOUES64 | 918119 | 385 | 3 - 317 | 1285 | Pro-89 to Leu-102. | | | AR061: 1, AR089: 0 S0040: 1 and S0278: 1. | | | |
| 376 | HWLHU02 | 918520 | 386 | 3 - 398 | 1286 | Gly-6 to Cys-12, Glu-48 to Asp-54, Ile-61 to Ser-73, Asn-75 to Thr-85, Gln-111 to Thr-118. | | | AR061: 2, AR089: 1 L0761: 2, L0791: 2, S0354: 1 and H0682: 1. | | | |
| 377 | HBAHA84 | 919363 | 387 | 84 - 794 | 1287 | Pro-20 to Ala-30. | | | AR089: 46, AR061: 9 | | | |
| 378 | HBMXQ90 | 922114 | 388 | 149 - 439 | 1288 | | | | AR089: 7, AR061: 6 S0116: 1, H0646: 1 and L0731: 1. | | | |
| 379 | HOEJV72 | 930778 | 389 | 77 - 817 | 1289 | Leu-51 to Asp-57, Leu-91 to Lys-97, Asp-143 to Pro-148. | | | AR089: 6, AR061: 5 S0360: 9, L0642: 5, L0752: 5, L0662: 4, L0659: 4, L0666: 4, S0007: 3, L0646: 3, L0776: 3, L0750: 3, H0662: 2, S0222: 2, L0483: 2, L0764: 2, L0648: 2, L0775: 2, L0665: 2, H0648: 2, | 104770, 107300, 107670, 110700, 131210, 136132, 145001, 146790, 150292, 159440, | | |

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| 380 | HRDBH58 | 933364 | 390 | 455 - 2239 | 1290 | L0779: 2, S0031: 2, S0110: 1, H0638: 1, S0418: 1, S0376: 1, S0444: 1, L0717: 1, H0331: 1, H0574: 1, S0414: 1, H0492: 1, H0156: 1, L0021: 1, S0049: 1, H0310: 1, H0327: 1, H0373: 1, T0010: 1, S6028: 1, H0615: 1, S0366: 1, S0036: 1, H0038: 1, H0616: 1, H0413: 1, T0041: 1, H0494: 1, S0438: 1, H0509: 1, S0142: 1, S0210: 1, L0598: 1, L0762: 1, L0640: 1, L0631: 1, L0772: 1, L0766: 1, L0551: 1, L0774: 1, L0664: 1, H0547: 1, S0126: 1, H0659: 1, S0378: 1, S0152: 1, S3014: 1, L0439: 1, L0740: 1, L0754: 1, L0756: 1, L0780: 1, L0755: 1, L0758: 1, S0434: 1, S0026: 1 and H0667: 1. | 159440, 159440, 173610, 186780, 191030, 191315, 208250, 233710, 600923, 600995, 601412, 601518, 601652, 602491 |
| | | | | | | AR089: 1, AR061: 0 | |

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| | | | | | | Arg-96 to Asn-104. | H0670: 3, H0261: 2, S0222: 2, L0771: 2, L0803: 2, S0358: 1, S0360: 1, H0632: 1, H0575: 1, H0615: 1, H0059: 1, H0509: 1, L0772: 1, L0646: 1, L0764: 1, L0662: 1, L0805: 1, L0776: 1 and L0596: 1. | | | |
| 383 | HFXJW08 | 959204 | 393 | 170 - 580 | 1293 | Val-12 to Arg-18, Thr-84 to Leu-90, Asp-103 to Gln-114. | AR089: 1, AR061: 0 S0282: 2 and H0135: 1. | | | |
| 384 | HBTAD04 | 407351 | 394 | 1 - 318 | 1294 | Ser-10 to Gln-18. | AR089: 1, AR061: 0 S0180: 1, H0416: 1 and S0028: 1. | | | |
| 385 | HE8FG51 | 465267 | 395 | 1 - 267 | 1295 | Gly-1 to Ile-8, Pro-10 to Asp-16, Asn-19 to Tyr-25, Gly-42 to Lys-49, Ile-59 to Gly-66. | AR061: 4, AR089: 1 H0266: 2, H0013: 1 and L0758: 1. | | | |
| 386 | HTPDU31 | 503077 | 396 | 305 - 3 | 1296 | Asp-3 to Gly-11. | AR061: 11, AR089: 8 S0007: 1, S0046: 1, H0052: 1, H0039: 1 and L0439: 1. | | | |
| 387 | HMUBV12 | 549423 | 397 | 64 - 306 | 1297 | | AR061: 2, AR089: 2 L0592: 2, H0013: 1, H0178: 1, H0099: 1, H0032: 1, H0529: 1, | 3p21.3 | 116806, 120120, 120120, 120120, | |

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| | | | | | | | | L0772: 1, H0521: 1 and L0780: 1. | | | 120436, 120436, 120436, 138320, 168468, 182280, 600163 |
| 388 | HMHBS90 | 574062 | 398 | 40 - 618 | 1298 | Arg-3 to Gln-14, Gln-25 to Glu-30. | | AR061: 3, AR089: 3 L0747: 9, L0794: 5, L0789: 4, L0662: 3, L0803: 3, S0152: 3, L0439: 3, L0777: 3, L0757: 3, L0593: 3, H0624: 2, H0318: 2, H0673: 2, H0412: 2, L0800: 2, L0764: 2, L0776: 2, L0748: 2, H0171: 1, T0049: 1, H0657: 1, H0661: 1, H0449: 1, H0580: 1, H0619: 1, H0370: 1, H0156: 1, H0253: 1, H0052: 1, H0620: 1, H0201: 1, S0051: 1, T0010: 1, H0286: 1, H0688: 1, H0622: 1, H0181: 1, L0456: 1, H0135: 1, H0087: 1, H0264: 1, L0065: 1, H0633: 1, S0144: 1, | | | |

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| 389 | HLHGH34 | 575733 | 399 | 2 - 436 | 1299 | Phe-10 to Asn-18, Leu-80 to Ile-86, Ile-118 to Arg-123. | S0142: 1, H0529: 1, L0763: 1, L0770: 1, L0769: 1, L0761: 1, L0643: 1, L0644: 1, L0773: 1, L0767: 1, L0766: 1, L0381: 1, L0527: 1, L0659: 1, L0809: 1, L0666: 1, H0519: 1, H0593: 1, H0689: 1, H0435: 1, H0670: 1, S0037: 1, S0027: 1, L0779: 1, L0752: 1, L0758: 1, L0759: 1, L0595: 1, S0106: 1 and H0422: 1. AR061: 5, AR089: 2 S0007: 2, H0024: 2, L0749: 2, S0003: 1, H0659: 1, L0748: 1, L0740: 1, L0758: 1 and L0595: 1. | 10p15.1 | | |
| 390 | HELHC55 | 577384 | 400 | 214 - 2 | 1300 | | AR061: 6, AR089: 2 S0001: 1 and S0045: 1. | | | |
| 391 | HKAAZ66 | 592105 | 401 | 3 - 434 | 1301 | Arg-1 to Phe-19, Gln-22 to Arg-28, Leu-92 to Thr-108. | AR089: 2, AR061: 1 L0659: 13, L0731: 12, L0803: 9, L0439: 9, L0601: 8, S0152: 7, L0756: 7, H0551: 6, L0666: 5, L0747: 5, L0646: 4, L0375: 4, | 1 | | |

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| | L0438: 4, H0519: 4, L0599: 4, L0600: 4, S0045: 3, H0013: 3, H0050: 3, H0622: 3, H0644: 3, H0494: 3, L0372: 3, L0662: 3, H0670: 3, H0660: 3, L0602: 3, H0521: 3, L0752: 3, L0757: 3, L0758: 3, S0212: 2, S0001: 2, S0046: 2, L0717: 2, H0266: 2, S0022: 2, H0031: 2, H0628: 2, H0264: 2, H0412: 2, L0770: 2, L0637: 2, L0649: 2, L0804: 2, L0378: 2, L0654: 2, L0655: 2, L0517: 2, H0689: 2, H0672: 2, H0539: 2, L0740: 2, L0754: 2, L0590: 2, H0265: 1, H0556: 1, S0040: 1, T0049: 1, S0116: 1, S0356: 1, S0354: 1, S0444: 1, S0360: 1, S0132: 1, H0549: 1, H0550: 1, H0438: 1, H0613: 1, H0486: 1, T0039: 1, T0040: 1, S0280: 1, L0021: 1, | |
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| | | | | | | | | S0378: 1, H0696: 1, H0704: 1, H0436: 1, S0390: 1, S3014: 1, S0028: 1, L0777: 1, L0755: 1, H0445: 1, L0588: 1, L0605: 1, L0485: 1, S0026: 1, S0192: 1, S0194: 1, H0542: 1, S0412: 1 and H0352: 1. | | | |
| 392 | HHSCN33 | 657367 | 402 | 1 - 396 | 1302 | | | AR089: 2, AR061: 1 H0013: 1, S0010: 1, S0051: 1 and L0741: 1. | | | |
| 393 | HNGJQ15 | 660310 | 403 | 1 - 207 | 1303 | His-51 to Gly-56. | | AR061: 8, AR089: 5 S0052: 1 and H0136: 1. | 2q37.2 | | |
| 394 | HDJME16 | 661396 | 404 | 1 - 486 | 1304 | Ser-8 to Ala-16, Leu-51 to Gln-56, Tyr-61 to Ala-73, Ala-77 to Thr-83, Gln-90 to Glu-104, Glu-118 to Asp-127. | | AR061: 1, AR089: 0 S0360: 2, H0553: 2, L0776: 2, L0744: 2, L0747: 2, L0750: 2, H0542: 2, S0110: 1, S0400: 1, H0441: 1, H0392: 1, H0156: 1, S0051: 1, H0687: 1, H0135: 1, H0087: 1, H0647: 1, L0631: 1, L0638: 1, L0774: 1, L0775: 1, L0659: 1, H0547: 1, S0380: 1, S0332: 1, L0743: 1, L0749: 1 and L0777: 1. | 3q21-q25 | 106165, 117700, 117700, 150210, 169600, 180380, 180380, 180380, 190000, 203500, 222900, 232050, 276902, 600882, 601199, | |

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| | | | | | | | | | 601199, 601199, 601471, 601682 | |
| 395 | HNTNR64 | 670033 | 405 | 3 - 365 | 1305 | Asp-19 to Trp-25. | | AR089: 1, AR061: 0 L0749: 8, L0759: 6, L0789: 3, L0748: 3, H0624: 2, L0471: 2, H0266: 2, H0170: 1, H0171: 1, S0360: 1, S0222: 1, H0441: 1, H0333: 1, H0013: 1, H0244: 1, H0251: 1, H0014: 1, H0553: 1, H0032: 1, S0036: 1, S0306: 1, S0150: 1, L0766: 1, L0653: 1, H0144: 1, H0520: 1, H0593: 1, H0690: 1, H0660: 1, S0380: 1, H0518: 1, H0521: 1, S0032: 1, L0439: 1, L0740: 1, L0751: 1, L0750: 1, L0756: 1, L0731: 1, L0589: 1, H0668: 1 and H0293: 1. | | |
| 396 | HMICO24 | 677036 | 406 | 1 - 303 | 1306 | Arg-7 to Trp-13, Thr-18 to Trp-29, Gly-55 to Ser-60. | | AR061: 9, AR089: 7 L0766: 9, L0731: 5, S6028: 2, L0779: 2, H0650: 1, S0001: 1, | | |

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| 397 | HSIAC23 | 679292 | 407 | 92 - 424 | 1307 | Arg-34 to Thr-40, Asp-79 to Gly-90. | AR061: 0, AR089: 0 L0439: 8, L0438: 7, L0666: 4, H0685: 1, S0376: 1, S0360: 1, L0444: 1, L0021: 1, H0036: 1, H0553: 1, L0772: 1, L0771: 1, L0768: 1, L0774: 1, L0651: 1, L0659: 1, H0684: 1, H0672: 1 and L0754: 1. | 9q21.11-21.33 | 602014 | |
| 398 | HSLFL74 | 685897 | 408 | 3 - 473 | 1308 | | AR089: 1, AR061: 0 S0028: 2, S0218: 1, S0001: 1 and S0390: 1. | | | |
| 399 | HSDJD53 | 698259 | 409 | 163 - 624 | 1309 | Ala-29 to Leu-35, Ala-45 to Pro-53, Ser-80 to Arg-89, Val-111 to Cys-118. | AR089: 2, AR061: 0 H0687: 2, S0050: 1, S0028: 1, S0031: 1 and S0260: 1. | | | |
| 400 | HCEBF33 | 702955 | 410 | 3 - 581 | 1310 | | AR061: 6, AR089: 4 L0439: 2, H0052: 1, | | | |

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| 401 | HAPQW27 | 705518 | 411 | 1 - 327 | 1311 | Asn-3 to Arg-11, Gln-42 to Asp-50. | H0644: 1, H0520: 1 and L0756: 1. AR061: 4, AR089: 1 L0748: 5, L0744: 4, L0751: 4, H0039: 3, H0617: 3, L0646: 3, L0809: 3, L0779: 3, H0295: 2, H0255: 2, S0358: 2, H0575: 2, H0457: 2, H0181: 2, H0673: 2, L0637: 2, L0743: 2, L0750: 2, L0758: 2, S0116: 1, H0663: 1, S0356: 1, S0376: 1, S0360: 1, H0675: 1, S0007: 1, H0497: 1, H0590: 1, H0618: 1, H0253: 1, H0545: 1, S0051: 1, H0622: 1, H0030: 1, H0135: 1, H0538: 1, S0426: 1, H0529: 1, L0763: 1, L0769: 1, L0764: 1, L0771: 1, L0773: 1, L0775: 1, L0788: 1, L0663: 1, H0144: 1, L0438: 1, H0690: 1, H0670: 1, H0672: 1, S0328: 1, S0406: 1, H0187: 1, | 8qter | |
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| 402 | HCFLZ28 | 707183 | 412 | 133 - 513 | 1312 | Glu-46 to Gly-54, Val-64 to Ala-69, Glu-74 to Leu-79, Glu-90 to Glu-97. | L0747: 1, L0749: 1, L0759: 1 and L0608: 1. AR089: 2, AR061: 1 H0556: 8, L0596: 8, L0588: 6, H0618: 5, H0266: 5, H0038: 5, H0616: 5, H0547: 5, L0740: 5, H0265: 4, S0022: 4, H0591: 4, H0529: 4, L0769: 4, L0766: 4, L0664: 4, H0521: 4, L0747: 4, S0420: 3, H0497: 3, H0253: 3, H0031: 3, H0135: 3, H0264: 3, H0056: 3, H0494: 3, L0657: 3, L0438: 3, L0748: 3, L0777: 3, L0758: 3, H0543: 3, H0624: 2, H0656: 2, S0418: 2, S0007: 2, H0333: 2, H0013: 2, S0010: 2, H0596: 2, L0471: 2, H0083: 2, H0039: 2, H0622: 2, H0617: 2, H0068: 2, H0163: 2, H0623: 2, H0100: 2, L0369: 2, L0763: 2, L0764: 2, L0378: 2, L0656: 2, | | | | |
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| | | L0663: 2, H0144: 2, H0701: 2, H0520: 2, H0690: 2, H0539: 2, H0478: 2, L0439: 2, L0750: 2, L0759: 2, L0593: 2, L0595: 2, H0653: 2, H0542: 2, H0170: 1, H0171: 1, S0402: 1, S0356: 1, S0358: 1, S0045: 1, S0046: 1, H0393: 1, L0717: 1, H0550: 1, S0222: 1, H0592: 1, H0587: 1, H0642: 1, T0114: 1, H0101: 1, T0082: 1, S0346: 1, H0318: 1, S0049: 1, T0115: 1, H0597: 1, H0530: 1, H0546: 1, H0050: 1, H0024: 1, H0015: 1, H0373: 1, H0286: 1, H0401: 1, H0553: 1, H0383: 1, H0673: 1, H0124: 1, S0366: 1, H0634: 1, H0551: 1, H0412: 1, H0413: 1, H0059: 1, H0102: 1, S0112: 1, L0475: 1, H0560: 1, S0150: 1, H0633: 1, H0538: 1, S0210: 1, | |
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| | | | | | | | | | L0770: 1, L0646: 1, L0773: 1, L0662: 1, L0768: 1, L0381: 1, L0803: 1, L0804: 1, L0651: 1, L0653: 1, L0606: 1, L0527: 1, L0659: 1, L0526: 1, L0519: 1, S0006: 1, S0374: 1, H0519: 1, S0126: 1, H0711: 1, S0328: 1, S0152: 1, H0696: 1, H0626: 1, H0627: 1, L0752: 1, L0755: 1, L0757: 1, H0445: 1, L0591: 1, L0581: 1, L0601: 1, H0665: 1, H0136: 1, S0192: 1, H0423: 1, L0697: 1, S0424: 1 and H0293: 1. | | | | |
| 403 | HWCAB58 | 710377 | 413 | 3 - 449 | 1313 | Lys-14 to Leu-21. | AR089: 13, AR061: 6 L0759: 2, H0012: 1, S0294: 1, L0809: 1, L0791: 1 and L0777: 1. H0255: 2, H0163: 1, H0691: 1 and L0747: 1. AR089: 2, AR061: 1 | | | | | | |
| 404 | HLMMC57 | 713770 | 414 | 221 - 478 | 1314 | | | | | | | | |
| 405 | HMEIHH37 | 717556 | 415 | 163 - 558 | 1315 | Asp-34 to Ser-44. | | | | | | | |
| 406 | HNGJI55 | 722240 | 416 | 1 - 303 | 1316 | Arg-1 to Asp-11, Thr-15 to Thr-21. | AR050: 48, AR054: 42, AR051: 37, AR061: | | | | | | |

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|-----|---------|--------|-----------|-----------|------|---|--|--|--|
| | | | | | | Pro-93 to Glu-101. | 6, AR089: 3 H0164: 1, S0052: 1 and S0031: 1. | | |
| | 868063 | 869 | 218 - 646 | 1769 | | His-8 to Gly-18, Glu-30 to Asp-36, Thr-40 to Thr-46, Pro-118 to Ala-133. | | | |
| 407 | HHGDG42 | 724795 | 417 | 128 - 358 | 1317 | | AR061: 47, AR089: 2 | | |
| 408 | HMTMF31 | 731302 | 418 | 50 - 424 | 1318 | | AR089: 1, AR061: 0 H0525: 1 | | |
| 409 | HSDIF59 | 739212 | 419 | 282 - 752 | 1319 | Pro-19 to Thr-31, Asp-137 to Ser-143. | AR089: 4, AR061: 2 S0218: 1, S0222: 1, H0617: 1, S0150: 1 and S0260: 1. | | |
| 410 | HNDAG60 | 751953 | 420 | 174 - 365 | 1320 | Ser-9 to Asp-15, Glu-20 to Asp-28, Glu-34 to Cys-40. | AR089: 14, AR061: 7 H0031: 2, H0624: 1, S0116: 1, S0354: 1, S0045: 1, H0581: 1, H0046: 1, H0428: 1, H0038: 1, H0494: 1, H0517: 1 and S0053: 1. | | |
| 411 | HSLDS79 | 753247 | 421 | 99 - 1646 | 1321 | Pro-5 to Lys-12, Ala-31 to Pro-41, Phe-58 to Thr-63, Gln-83 to Phe-89, Pro-102 to Leu-116, Ser-130 to Asp-138, Pro-196 to Gln-208, Tyr-231 to Ala-240, | AR050: 10, AR051: 4, AR054: 3, AR089: 1, AR061: 1 H0544: 1 and S0028: 1. | | |

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|-----|---------|--|--|--|--|--------|--|----------|------|--|---|
| | | | | | | | Gly-252 to Arg-257, Arg-269 to Ser-281, Ala-289 to Ala-297, Phe-314 to Thr-327, Ala-371 to Ile-376, Tyr-379 to Trp-387, Lys-394 to Asn-400, Lys-443 to Gly-453, Asp-490 to Glu-497, Val-510 to Glu-516. | | | | |
| | | | | | | 879215 | 870 | 349 - 2 | 1770 | Asn-31 to Ser-38, Pro-82 to Thr-89. | |
| 412 | HFBCQ61 | | | | | 769102 | 422 | 3 - 245 | 1322 | Glu-9 to Trp-18. | H0590: 1 and N0006: 1. |
| 413 | HRACD17 | | | | | 769103 | 423 | 2 - 385 | 1323 | Phe-1 to Lys-7, Met-14 to Gly-20. | AR089: 1, AR061: 1 S6028: 2, H0553: 2, L0766: 2, L0754: 2, H0650: 1, S0001: 1, H0663: 1, T0048: 1, H0050: 1, S0003: 1, H0551: 1, H0412: 1, S0426: 1, H0365: 1, H0539: 1, H0555: 1, L0740: 1, L0777: 1 and L0757: 1. |
| 414 | HLDQV23 | | | | | 788957 | 424 | 17 - 376 | 1324 | Ala-55 to Ser-60, His-83 to Gly-90. | AR061: 2, AR089: 2 S0052: 3, L0438: 3, H0063: 2, H0144: 2, L0439: 2, L0587: 2, S0342: 1, L0785: 1, |

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| | | | | | | | | | T0082: 1, H0009: 1, H0083: 1, H0510: 1, H0266: 1, H0135: 1, T0041: 1, H0494: 1, L0369: 1, L0667: 1, L0800: 1, L0774: 1, L0787: 1, H0547: 1, L0747: 1, L0759: 1, L0593: 1 and S0424: 1. | | |
| 415 | HPHAF45 | 812327 | 425 | 1 - 384 | 1325 | Cys-26 to Trp-34, Phe-111 to Asp-119. | | | AR089: 1, AR061: 0 H0619: 1, H0431: 1, S0148: 1, H0519: 1, L0589: 1, L0591: 1 and L0594: 1. | | |
| 416 | HSUME31 | 812373 | 426 | 1 - 441 | 1326 | Thr-2 to Arg-7, Asp-37 to Trp-42. | | | AR061: 168, AR089: 115 H0556: 6, H0265: 4, H0040: 4, S0418: 2, S0420: 2, H0266: 2, H0038: 2, T0002: 1, T0049: 1, S0045: 1, S0046: 1, S0022: 1, H0256: 1, H0486: 1, H0634: 1, L0766: 1, S0052: 1, S0126: 1, H0539: 1, S0037: 1, S0027: 1, L0743: 1, L0751: 1, L0749: 1, L0731: 1, L0591: 1, L0595: 1, H0136: 1, | | |

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| 417 | HUSHB56 | 815819 | 427 | 2 - 412 | 1327 | Pro-8 to Arg-14, Glu-16 to Arg-23, Gly-25 to Pro-30, Arg-59 to Glu-69, Pro-78 to Glu-83. | S0276: 1 and H0543: 1. AR089: 2, AR061: 1 H0437: 1 and H0538: 1. | | |
| 418 | HTGDN81 | 824708 | 428 | 390 - 1031 | 1328 | | AR050: 9, AR054: 3, AR051: 1, AR061: 0, AR089: 0 S0028: 2, S0134: 1, S0132: 1 and S0222: 1. | | |
| 419 | HSKHY26 | 836598 | 429 | 2 - 571 | 1329 | | AR089: 1, AR061: 0 H0478: 3, S0278: 2, L0731: 2, S0001: 1, S0360: 1, S0132: 1, H0619: 1, H0263: 1, S0036: 1, H0040: 1, H0494: 1, S0142: 1, S0344: 1, L0764: 1, L0766: 1, S014: 1, L0748: 1, H0445: 1 and S0434: 1. | 12q13 | 10777, 123940, 139350, 139350, 148040, 148041, 148043, 148070, 231550, 600194, 600231, 600536, 600808, 600956, 601284, 601769, 601769, 601928, 602116, |

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| 420 | HKACD80 | 837698 | 430 | 72 - 536 | 1330 | Pro-34 to Val-40, Thr-65 to Asp-70. | AR089: 12, AR061: 6 L0766: 4, H0052: 3, L0662: 3, L0776: 3, L0666: 3, L0665: 3, H0521: 3, H0438: 2, H0581: 2, H0263: 2, H0494: 2, L0763: 2, L0770: 2, L0769: 2, L0649: 2, L0664: 2, L0748: 2, L0439: 2, L0747: 2, S0436: 2, H0265: 1, H0556: 1, S0040: 1, H0656: 1, S0444: 1, S0278: 1, H0415: 1, H0403: 1, H0643: 1, S0280: 1, H0575: 1, H0194: 1, H0309: 1, H0545: 1, H0046: 1, L0157: 1, H0375: 1, L0483: 1, H0553: 1, H0412: 1, H0646: 1, S0002: 1, L0796: 1, L0644: 1, L0764: 1, L0774: 1, L0376: 1, L0806: 1, L0654: 1, L0659: 1, L0383: 1, H0547: 1, S0126: 1, H0684: 1, H0435: 1, H0478: 1, | | 602153 |
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| | | | | | | | | S0028: 1, L0751: 1, L0754: 1, L0749: 1, L0750: 1, L0779: 1, L0759: 1, H0543: 1 and H0423: 1. | | | |
| 421 | HHFDK48 | 837782 | 431 | 1 - 384 | 1331 | Asn-1 to Gly-8, His-10 to Lys-15, Gly-96 to Cys-102, Pro-104 to Phe-109. | | AR089: 257, AR061: 210 H0050: 1, L0194: 1 and H0555: 1. | | | |
| 422 | HE9SS77 | 838043 | 432 | 3 - 725 | 1332 | Leu-1 to Tyr-8, Lys-21 to Asn-27, Asn-33 to Thr-49. | | AR089: 102, AR061: 58 H0013: 1, S0250: 1, S0022: 1, H0038: 1, L0659: 1, H0144: 1 and S0390: 1. | | | |
| 423 | HAPOK49 | 848205 | 433 | 123 - 1031 | 1333 | | | AR061: 8, AR089: 6 H0641: 9, L0748: 6, L0731: 5, L0777: 4, L0758: 4, L0771: 3, L0755: 3, H0638: 2, H0622: 2, L0769: 2, L0637: 2, L0662: 2, L0766: 2, L0775: 2, S0126: 2, H0518: 2, H0521: 2, H0522: 2, S0206: 2, L0779: 2, H0423: 2, T0002: 1, H0657: 1, L0785: 1, H0661: 1, L0562: 1, L0539: 1, S0356: 1, | | | |

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| | | | | | | | | | L0622: 1, H0486: 1, H0427: 1, H0575: 1, H0004: 1, H0083: 1, H0109: 1, H0039: 1, H0617: 1, H0090: 1, H0063: 1, H0130: 1, S0002: 1, S0426: 1, L0763: 1, L0770: 1, L0761: 1, L0772: 1, L0372: 1, L0764: 1, L0768: 1, L0774: 1, L0776: 1, L0655: 1, L0659: 1, L0542: 1, L0789: 1, L0666: 1, L0663: 1, L0438: 1, H0435: 1, S0044: 1, S0404: 1, H0187: 1, H0478: 1, L0747: 1, L0759: 1, L0591: 1 and H0543: 1. | | | | |
| 424 | HPMGN48 | 848318 | 434 | 3 - 635 | 1334 | His-1 to Thr-6, Pro-14 to Trp-21, Glu-43 to Gly-50, Asp-97 to Gly-103, Glu-141 to Asp-149, Ile-199 to Gly-204. | | AR089: 15, AR061: 5, H0550: 2, L0662: 2, H0657: 1, H0662: 1, H0619: 1, S0474: 1, H0081: 1, L0471: 1, H0428: 1, H0031: 1, H0063: 1, H0494: 1, L0642: 1, L0666: 1, L0748: 1 and L0747: 1. | | | | | |
| 425 | HUVHP54 | 849278 | 435 | 258 - 1001 | 1335 | Glu-86 to Asp-93, | | AR061: 7, AR089: 7 | | | | | |

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| 426 | HSLDK59 | 853385 | 436 | 491 - 1009 | 1336 | Glu-18 to Lys-24, Pro-68 to Gly-75, Tyr-122 to Arg-136, Pro-148 to Glu-158. | Trp-100 to Asp-110, Asp-163 to Asn-172. | S0358: 5, H0590: 2, H0623: 2, L0803: 2, S0152: 2, S3014: 2, L0754: 2, H0458: 1, S0354: 1, H0549: 1, H0431: 1, H0497: 1, H0042: 1, H0036: 1, H0581: 1, H0196: 1, T0115: 1, H0024: 1, H0275: 1, H0622: 1, S0364: 1, H0124: 1, H0056: 1, H0429: 1, S0150: 1, L0640: 1, L0642: 1, L0804: 1, L0666: 1, S0330: 1, H0478: 1, S0027: 1, S0206: 1, L0592: 1, L0604: 1 and S0424: 1. | | |
| 427 | HMWDI41 | 854051 | 437 | 2 - 613 | 1337 | Ile-30 to Cys-36, Pro-56 to Gly-65, Glu-105 to Glu-110. | | AR061: 1, AR089: 1 S0028: 3, S0222: 2, L0105: 2, S0050: 2, S0390: 2, S0260: 2, H0344: 1, H0381: 1, S0282: 1, H0618: 1, S0051: 1, S6028: 1, H0271: 1, H0383: 1, H0264: 1 and S0038: 1. | | |

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| 428 | HFVHU73 | 856165 | 438 | 3 - 314 | 1338 | Val-34 to Lys-56, Pro-65 to Asp-73, Thr-79 to Asn-84. | Tyr-170 to Arg-175, Asp-183 to Trp-189. | H0341: 1, S0358: 1, H0051: 1, S0210: 1, H0529: 1, L0803: 1, H0539: 1, H0521: 1, H0436: 1, L0779: 1, L0366: 1 and H0506: 1. AR089: 6, AR061: 1 H0341: 1, H0393: 1 and H0266: 1. | | |
| 429 | HMUBJ80 | 858497 | 439 | 517 - 2 | 1339 | | | AR089: 16, AR061: 4 L0748: 9, L0439: 5, L0717: 4, L0659: 4, L0663: 4, H0658: 4, S0045: 3, L0766: 3, L0744: 3, L0749: 3, L0758: 3, H0542: 3, H0265: 2, H0556: 2, S0040: 2, H0458: 2, H0587: 2, H0486: 2, H0318: 2, H0052: 2, H0687: 2, L0770: 2, L0769: 2, L0646: 2, L0666: 2, H0682: 2, L0756: 2, L0752: 2, L0731: 2, L0608: 2, H0543: 2, H0423: 2, H0656: 1, H0402: 1, S0418: 1, S0420: 1, S0360: 1, H0619: 1, H0392: 1, H0643: 1. | | |

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| Phe-131 to Lys-136, Pro-143 to Pro-149, Lys-189 to Leu-200, Asn-305 to Trp-310. | L0663: 4, L0754: 4, L0747: 4, L0804: 3, H0144: 3, L0750: 3, L0756: 3, L0752: 3, L0600: 3, S0003: 2, L0455: 2, S0366: 2, H0529: 2, L0659: 2, L0809: 2, L0665: 2, H0547: 2, H0672: 2, H0539: 2, L0748: 2, L0759: 2, L0591: 2, L0485: 2, S0040: 1, H0650: 1, H0656: 1, S0212: 1, H0663: 1, S0360: 1, H0351: 1, S0222: 1, S6014: 1, H0392: 1, H0632: 1, T0114: 1, H0427: 1, L0021: 1, H0599: 1, H0575: 1, H0581: 1, S0049: 1, L0471: 1, H0373: 1, H0510: 1, S6028: 1, H0615: 1, H0622: 1, S0036: 1, T0067: 1, H0413: 1, T0041: 1, S0002: 1, S0426: 1, L0369: 1, L0770: 1, L0769: 1, L0761: 1, L0772: 1, L0646: 1, L0794: 1, L0774: 1, L0775: 1. |
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| | | | | | | | L0655: 1, L0661: 1, L0647: 1, L0792: 1, L0793: 1, L0664: 1, H0682: 1, H0435: 1, H0659: 1, H0660: 1, H0651: 1, S0013: 1, H0436: 1, L0779: 1, L0608: 1, S0446: 1 and H0506: 1. | | | |
| 431 | HLQAJ01 | 864092 | 441 | 1 - 300 | 1341 | Pro-56 to Arg-67, Asp-86 to Gly-98. | AR089: 14, AR061: 10 L0803: 4, L0764: 2, L0794: 2, H0331: 1, H0574: 1, H0486: 1, H0318: 1, H0264: 1, L0804: 1, L0809: 1, L0665: 1, L0438: 1, H0684: 1, L0759: 1 and L0584: 1. | | | |
| 432 | HSLDP32 | 866241 | 442 | 12 - 257 | 1342 | Asn-6 to Lys-13. | AR089: 1, AR061: 0 S0028: 2, H0135: 1, H0163: 1 and S0044: 1. | | | |
| 433 | HPMEG40 | 866272 | 443 | 270 - 611 | 1343 | Val-1 to Leu-7, Arg-49 to Trp-59. | AR089: 0, AR061: 0 S0028: 4, S0390: 2, S0300: 1, H0031: 1, S0144: 1 and S0032: 1. | | | |
| 434 | HRADE27 | 867195 | 444 | 2 - 547 | 1344 | Glu-33 to Pro-38. | AR089: 1, AR061: 0 L0435: 2, H0624: 1, L0717: 1, S0214: 1, L0662: 1, L0766: 1, L0803: 1, S0380: 1, | | | |

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| 435 | HTXQR10 | 869137 | 445 | 76 - 537 | 1345 | Ser-38 to Thr-46. | AR061: 5, AR089: 3 H0250: 4, L0745: 4, L0746: 4, L0766: 3, L0666: 2, L0758: 2, H0556: 1, S0418: 1, H0486: 1, H0052: 1, H0252: 1, H0181: 1, H0116: 1, H0412: 1, S0210: 1, L0764: 1, L0794: 1 and H0672: 1. | H0555: 1, L0754: 1 and L0756: 1. | |
| 436 | HBQCB27 | 871062 | 446 | 1 - 423 | 1346 | | AR089: 19, AR061: 3 H0544: 1 and S0036: 1. | | |
| 437 | HB8AM04 | 871156 | 447 | 3 - 518 | 1347 | | AR061: 223, AR089: 167 H0013: 2, H0135: 1 and H0633: 1. | | |
| 438 | HSLHT48 | 871996 | 448 | 81 - 542 | 1348 | Pro-17 to Ala-22. | AR061: 1, AR089: 1 S0028: 2, S0045: 1, S6026: 1, H0231: 1, S0050: 1, H0617: 1, H0189: 1 and S0144: 1. | | |
| 439 | HS2SH70 | 875870 | 449 | 193 - 1014 | 1349 | Thr-5 to Gln-52, Lys-121 to Ile-134. | AR089: 1, AR061: 1 H0124: 5, T0040: 2, H0144: 2, S0342: 1, S0046: 1, H0550: 1, H0455: 1, H0486: 1, H0575: 1, T0110: 1, H0046: 1, H0266: 1. | | |

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| | | | | | | | | | H0316: 1, H0616: 1, H0551: 1, T0041: 1, H0561: 1, L0438: 1, H0547: 1, S0152: 1, H0521: 1, H0555: 1, H0631: 1 and L0731: 1. | | | |
| 440 | HAOAE45 | 876157 | 450 | 3 - 440 | 1350 | | | | AR089: 414, AR061: 79 L0751: 2, H0341: 1, S0132: 1, H0550: 1, S0222: 1, H0431: 1, H0046: 1, L0471: 1, H0083: 1, S0314: 1, H0031: 1, H0644: 1, H0488: 1, H0413: 1, T0041: 1, S0150: 1, S0344: 1, L0662: 1, L0657: 1, L0663: 1, S0374: 1, H0519: 1, L0748: 1 and L0592: 1. | | | |
| 441 | HELBA42 | 878549 | 451 | 69 - 695 | 1351 | | | Lys-35 to Gln-40, Gln-61 to Lys-66, Ser-116 to Gly-121, Gln-192 to Ser-205. | AR089: 53, AR050: 32, AR054: 28, AR051: 24, AR061: 19 L0439: 3, S0212: 2, H0052: 2, S0051: 2, L0805: 2, H0435: 2, H0624: 1, H0265: 1, H0686: 1, S0420: 1, S0045: 1, S0300: 1, S0222: 1, H0069: 1, | | | |

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| | | | | | | | | H0381: 1, L0157: 1, T0010: 1, H0355: 1, H0266: 1, H0428: 1, T0041: 1, L0475: 1, H0130: 1, S0210: 1, S0002: 1, L0788: 1 and L0759: 1. | | | |
| 442 | HSPBB15 | 878791 | 452 | 1 - 564 | 1352 | Gly-19 to Thr-24. | | AR089: 10, AR061: 2 H0484: 2, H0052: 1 and H0478: 1. | | | |
| 443 | HTAFF91 | 879399 | 453 | 3 - 431 | 1353 | Gly-1 to Cys-6. | | AR089: 4, AR061: 0 H0305: 2, H0587: 1 and H0069: 1. | | | |
| 444 | HETHB58 | 879640 | 454 | 28 - 669 | 1354 | Ser-28 to Val-35, Arg-49 to Arg-57. | | AR061: 4, AR089: 2 H0539: 5, L0758: 4, H0620: 3, L0809: 3, H0050: 2, S0002: 2, L0803: 2, L0805: 2, S0330: 2, L0754: 2, L0755: 2, L0605: 2, H0265: 1, H0556: 1, S0040: 1, H0341: 1, S0212: 1, S0110: 1, S0360: 1, H0645: 1, S0278: 1, H0431: 1, H0497: 1, H0013: 1, H0618: 1, H0581: 1, H0052: 1, H0544: 1, H0046: 1, H0024: 1, H0051: 1, S0250: 1, | | | |

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| 445 | HGBCU40 | 880328 | 455 | 93 - 533 | 1355 | Pro-1 to Lys-12, Gln-29 to Arg-34, Asn-37 to Tyr-48, Asn-54 to Ser-63, Pro-68 to Leu-73, Asp-125 to Gln-135. | S0022: 1, H0622: 1, L0142: 1, H0124: 1, S0344: 1, L0770: 1, L0761: 1, L0794: 1, L0774: 1, L0776: 1, L0656: 1, L0659: 1, L0789: 1, L0666: 1, L0665: 1, S0428: 1, H0519: 1, S0126: 1, H0435: 1, H0555: 1, S3014: 1, S0028: 1, L0756: 1, L0777: 1, S0031: 1, H0445: 1 and L0596: 1. | | |
| 446 | HE9PR39 | 882939 | 456 | 3 - 500 | 1356 | Pro-8 to Gly-17, Arg-22 to Ser-29. | AR089: 2, AR061: 1 H0251: 4, H0024: 2, H0341: 1, S0418: 1, H0015: 1, S0013: 1 and L0601: 1. | | |
| 447 | HTEAF36 | 839516 | 457 | 68 - 316 | 1357 | | AR061: 4, AR089: 2 H0013: 4, L0740: 3, H0163: 2, L0768: 2, L0593: 2, H0624: 1, H0171: 1, S0003: 1, T0006: 1, L0776: 1, H0144: 1, H0547: 1, L0750: 1, L0759: 1 and L0592: 1. | | |

H0529: 16, S0358: 14,
H0494: 14, L0755: 14,
L0665: 11, L0747: 11,
L0752: 11, H0521: 10,
S0360: 8, L0662: 8,
L0659: 8, H0435: 8,
L0439: 8, L0649: 7,
L0754: 7, L0601: 7,
H0663: 6, S0376: 6,
H0618: 6, L0637: 6,
L0646: 6, L0766: 6,
L0666: 6, H0295: 5,
H0661: 5, T0023: 5,
L0653: 5, S0380: 5,
L0758: 5, S0356: 4,
H0592: 4, H0586: 4,
H0497: 4, H0604: 4,
H0038: 4, L0772: 4,
L0768: 4, L0657: 4,
S0374: 4, H0685: 3,
S0442: 3, S0444: 3,
H0580: 3, H0253: 3,
H0581: 3, H0620: 3,
H0615: 3, H0031: 3,
H0617: 3, H0488: 3,
H0641: 3, H0647: 3,
L0794: 3, L0664: 3,
H0593: 3, L0748: 3,
L0750: 3, L0596: 3,
H0294: 2, H0656: 2,
H0483: 2, H0664: 2,

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S0354: 2, H0676: 2,
S0408: 2, H0392: 2,
H0409: 2, H0046: 2,
H0009: 2, H0012: 2,
H0083: 2, H0688: 2,
H0213: 2, H0030: 2,
H0264: 2, H0059: 2,
H0633: 2, S0422: 2,
L0763: 2, L0771: 2,
L0382: 2, H0144: 2,
S0310: 2, H0689: 2,
H0658: 2, H0670: 2,
H0660: 2, H0666: 2,
S0328: 2, S0330: 2,
H0696: 2, H0478: 2,
L0744: 2, L0749: 2,
L0731: 2, L0759: 2,
H0543: 2, S0424: 2,
H0556: 1, H0657: 1,
S0116: 1, H0484: 1,
H0662: 1, T0008: 1,
H0550: 1, H0370: 1,
H0587: 1, H0486: 1,
T0114: 1, L0021: 1,
H0318: 1, H0309: 1,
H0263: 1, H0234: 1,
H0596: 1, H0597: 1,
H0121: 1, H0150: 1,
L0471: 1, H0375: 1,
H0428: 1, H0033: 1,
H0644: 1, H0032: 1,

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H0673: 1, H0169: 1,
H0674: 1, S0036: 1,
H0040: 1, H0616: 1,
T0067: 1, H0560: 1,
H0625: 1, S0466: 1,
S0440: 1, S0150: 1,
S0472: 1, S0144: 1,
S0002: 1, L0640: 1,
L0770: 1, L0761: 1,
L0764: 1, L0363: 1,
L0364: 1, L0774: 1,
L0775: 1, L0375: 1,
L0806: 1, L0805: 1,
L0776: 1, L0655: 1,
L0493: 1, L0636: 1,
L0383: 1, L0809: 1,
L0663: 1, S0052: 1,
H0693: 1, H0547: 1,
S0126: 1, H0690: 1,
H0682: 1, H0683: 1,
H0684: 1, H0659: 1,
H0648: 1, H0672: 1,
S0152: 1, S0350: 1,
H0522: 1, S0392: 1,
S0432: 1, L0741: 1,
L0751: 1, L0745: 1,
L0757: 1, S0434: 1,
S0436: 1, L0592: 1,
L0599: 1, L0361: 1,
L0603: 1, S0460: 1,
S0446: 1, H0506: 1 and

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| 448 | HTLGV66 | 839517 | 871 | 253 - 501 | 1771 | Leu-21 to Phe-27, Gly-61 to Ala-68, Ala-85 to His-91, Asp-96 to Val-101, Asp-117 to Ile-131, Ala-155 to Ser-161. | L0600: 1. | | |
| | | 883195 | 872 | 1 - 669 | 1772 | | | | |
| 448 | HTLGV66 | 883855 | 458 | 3 - 1085 | 1358 | Glu-1 to Gln-19, Arg-58 to Pro-67, Glu-78 to Phe-85, Ser-104 to Arg-114, Arg-121 to Lys-130, Arg-135 to Thr-140, Asn-159 to Ser-168. | AR061: 1, AR089: 1 L0601: 2, H0618: 1, H0085: 1 and H0024: 1. | 2q37.2 | |
| 449 | HPJDV95 | 888844 | 459 | 362 - 1906 | 1359 | Thr-12 to Ser-19, Val-22 to Glu-32, His-34 to Lys-43, Glu-129 to Lys-134, Phe-221 to Gln-226, Pro-231 to Pro-236, Lys-288 to Lys-299, Glu-320 to Gln-327, Thr-448 to Pro-455, Thr-490 to Glu-495. | AR061: 6, AR089: 2 H0457: 5, L0439: 4, H0013: 3, H0244: 3, H0266: 3, L0748: 3, H0556: 2, H0052: 2, H0040: 2, L0741: 2, L0740: 2, L0747: 2, L0759: 2, H0543: 2, H0265: 1, S0356: 1, H0580: 1, S0132: 1, H0619: 1, S0222: 1, T0082: 1, H0036: 1, H0421: 1, H0046: 1, H0009: 1, H0620: 1, T0010: 1, H0083: 1, | | |

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| 450 | HCROF75 | 889436 | 460 | 48 - 533 | 1360 | Ser-14 to Trp-22. | | H0179: 1, H0271: 1, H0416: 1, S0250: 1, H0168: 1, H0634: 1, H0551: 1, S0386: 1, T0042: 1, H0641: 1, S0344: 1, L0766: 1, L0776: 1, L0565: 1, H0539: 1, S0152: 1, H0478: 1, L0754: 1, L0755: 1, H0707: 1, L0596: 1, L0605: 1, L0599: 1, H0542: 1, H0423: 1, H0422: 1 and H0506: 1. | | |
| 451 | HDPAP15 | 909703 | 461 | 131 - 1120 | 1361 | Arg-147 to Asn-153, Arg-165 to Glu-174, Phe-217 to Lys-222, Ala-306 to Ser-313. | | AR089: 29, AR061: 15 L0742: 2, S0356: 1, S0358: 1, S0360: 1, H0617: 1, H0040: 1 and H0522: 1. AR089: 5, AR061: 2 L0755: 6, H0521: 5, H0634: 4, L0771: 4, L0766: 4, L0759: 4, L0800: 3, L0774: 3, H0659: 3, L0748: 3, L0754: 3, H0171: 2, H0550: 2, H0587: 2, H0264: 2, L0764: 2, L0768: 2, L0803: 2, L0775: 2, L0517: 2 | | |

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| 452 | HTGDH34 | 896571 | 462 | 261 - 112 | 1362 | Lys-6 to Gly-12. | L0746: 1, L0747: 1, L0750: 1, L0757: 1, L0758: 1, H0445: 1, S0026: 1 and S0276: 1. AR089: 10, AR061: 6 L0766: 10, L0758: 10, L0755: 8, L0731: 6, H0616: 5, L0740: 5, H0494: 4, H0696: 4, L0756: 4, L0752: 4, L0757: 4, S0358: 3, H0038: 3, L0770: 3, L0775: 3, S0328: 3, L0747: 3, H0662: 2, H0638: 2, H0580: 2, S0280: 2, H0052: 2, H0266: 2, T0067: 2, L0809: 2, L0666: 2, S0126: 2, H0435: 2, H0648: 2, H0521: 2, L0744: 2, L0748: 2, L0751: 2, L0749: 2, L0750: 2, L0684: 2, H0423: 2, S0040: 1, S0134: 1, H0657: 1, H0341: 1, S0212: 1, H0125: 1, H0370: 1, H0587: 1, H0486: 1, T0109: 1, H0250: 1, L0021: 1, H0098: 1 | | | |
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| 453 | HPDEH29 | 913378 | 873 | 337 - 774 | 1773 | Pe-94 to Gly-99. | S0010: 1, H0581: 1, H0421: 1, H0251: 1, L0471: 1, H0057: 1, H0083: 1, H0428: 1, S0364: 1, S0366: 1, H0090: 1, H0412: 1, H0022: 1, S0422: 1, S0002: 1, L0520: 1, L0762: 1, L0763: 1, L0646: 1, L0764: 1, L0771: 1, L0662: 1, L0386: 1, L0774: 1, L0378: 1, L0805: 1, L0653: 1, L0776: 1, L0606: 1, L0628: 1, L0657: 1, L0659: 1, L0783: 1, L0792: 1, L0663: 1, H0547: 1, H0519: 1, H0672: 1, S0330: 1, H0539: 1, S0378: 1, S0136: 1, H0134: 1, S0027: 1, L0754: 1, L0759: 1, H0445: 1, H0707: 1, L0588: 1, L0366: 1, H0668: 1, S0026: 1, S0276: 1 and H0506: 1. | AR089: 1, AR061: 1 S0358: 4 L0748: 3 |
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| 454 | HDPVG08 | 914973 | 464 | 3 - 1715 | 1364 | Val-6 to Arg-16, Asp-25 to Thr-34. | L0764: 2, L0751: 2, H0295: 1, H0662: 1, H0240: 1, H0241: 1, H0675: 1, L0717: 1, S0222: 1, H0441: 1, H0036: 1, H0253: 1, T0023: 1, S0038: 1, L0662: 1, H0547: 1, H0555: 1, L0743: 1, L0749: 1 and L0758: 1. | 1q32 | 114208, 114208, 119300, 120620, 120620, 120920, 134370, 134370, 134370, 134580, 145260, 150310, 150310, 179820, 191045, 600105, 600759, 601494, 601975 |
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| H0622: 2, H0031: 2, H0628: 2, H0591: 2, H0038: 2, T0041: 2, S0422: 2, L0640: 2, L0638: 2, L0772: 2, L0662: 2, L0804: 2, L0784: 2, L0659: 2, L0517: 2, L0519: 2, S0052: 2, S0126: 2, L0745: 2, L0750: 2, L0780: 2, L0605: 2, H0395: 1, S0114: 1, H0664: 1, H0638: 1, S0348: 1, S0418: 1, S0444: 1, H0645: 1, H0393: 1, H0613: 1, H0587: 1, H0643: 1, H0574: 1, H0250: 1, H0069: 1, S0346: 1, S0049: 1, H0052: 1, H0596: 1, H0123: 1, L0471: 1, S0388: 1, S0214: 1, H0428: 1, H0030: 1, H0617: 1, H0032: 1, H0673: 1, L0455: 1, H0598: 1, H0634: 1, H0616: 1, H0264: 1, H0413: 1, H0059: 1, H0131: 1, H0641: 1, S0210: 1, H0529: 1, L0763: 1. |
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| | | | | | | | | | L0761: 1, L0764: 1, L0771: 1, L0521: 1, L0649: 1, L0650: 1, L0661: 1, L0384: 1, L0809: 1, L0647: 1, L0788: 1, L0789: 1, L0666: 1, L0663: 1, L0665: 1, S0428: 1, S0374: 1, H0519: 1, H0658: 1, H0648: 1, S0328: 1, S0330: 1, S0152: 1, H0696: 1, S0044: 1, H0436: 1, H0478: 1, H0540: 1, L0752: 1, L0753: 1, L0759: 1, S0031: 1, H0707: 1, L0608: 1, L0595: 1, S0026: 1, H0423: 1, L0697: 1, S0424: 1 and H0506: 1. | | | | |
| 455 | HFXDW32 | 916095 | 465 | 2 - 886 | 1365 | Gly-11 to Lys-20, His-41 to Cys-47, Thr-82 to Lys-90. | | | S0001: 2, H0624: 1, H0689: 1 and S0028: 1. | | | | |
| 456 | HSSCY03 | 916445 | 466 | 2 - 1345 | 1366 | | | | L0741: 4, L0744: 4, H0556: 3, S0344: 3, L0763: 3, L0766: 3, L0743: 3, L0754: 3, L0747: 3, L0758: 3, L0596: 3, S0212: 2, H0662: 2, S0358: 2, | | | | |

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| 457 | HFXFI49 | 916758 | 467 | 139 - 615 | 1367 | Lys-20 to Ile-29, Arg-46 to Pro-59, Ile-86 to Asn-93, Phe-115 to Asn-120. | AR061: 2, AR089: 1 S0028: 4, S0001: 2, S0282: 2, S0278: 2, S0050: 2, H0416: 1, H0027: 1, S0038: 1, S0052: 1, S0053: 1, H0684: 1 and S0044: 1. | | |
| | | | | | | | S0045: 2, S0140: 2, H0370: 2, L0483: 2, L0769: 2, L0774: 2, H0521: 2, L0748: 2, L0759: 2, S0114: 1, H0255: 1, H0306: 1, S0046: 1, H0619: 1, S0278: 1, S0280: 1, H0309: 1, T0010: 1, S6028: 1, H0424: 1, H0644: 1, S0036: 1, H0135: 1, H0272: 1, H0412: 1, H0059: 1, H0560: 1, H0561: 1, H0131: 1, H0647: 1, H0649: 1, L0770: 1, L0761: 1, L0776: 1, H0144: 1, H0672: 1, H0576: 1, S3014: 1, S0027: 1, L0749: 1, L0755: 1, S0026: 1, H0665: 1, S0196: 1 and H0506: 1. | | |

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| 458 | HTLGH72 | 917526 | 468 | 33 - 776 | 1368 | | AR089: 15, AR061: 11 L0803: 16, S0358: 2, H0031: 2, S0144: 2, L0770: 2, L0804: 2, L0439: 2, L0780: 2, S0116: 1, S0360: 1, H0441: 1, H0431: 1, H0331: 1, H0618: 1, H0544: 1, L0471: 1, H0510: 1, S0318: 1, H0264: 1, L0769: 1, L0783: 1, L0809: 1, L0790: 1, L0438: 1, L0355: 1, L0751: 1, L0779: 1, L0777: 1 and L0758: 1. | | |
| 459 | HSUAE63 | 917758 | 469 | 896 - 2188 | 1369 | Ser-2 to Gln-22, Pro-94 to His-110, Phe-167 to Ala-172, Leu-261 to Gly-268. | AR061: 2, AR089: 1 L0595: 6, H0069: 4, H0521: 4, L0777: 3, H0663: 2, H0620: 2, H0494: 2, L0646: 2, L0764: 2, L0649: 2, S0152: 2, L0592: 2, T0002: 1, S0040: 1, H0657: 1, H0341: 1, H0661: 1, H0305: 1, H0580: 1, H0645: 1, L0717: 1, H0431: 1, H0587: 1, T0040: 1, H0635: 1, H0575: 1, | | |

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| 460 | HAPTQ56 | 918920 | 470 | 1400 - 606 | 1370 | His-6 to Gly-16. | AR089: 233, AR061: 50 L0803: 7, L0766: 3, L0774: 3, L0659: 3, L0745: 3, L0791: 2, L0608: 2, S0356: 1, S0354: 1, S0376: 1, S0222: 1, H0013: 1, L0021: 1, H0575: 1, H0596: 1, H0457: 1, L0157: 1, S0003: 1, H0560: 1, H0130: 1, H0646: 1, S0142: 1, S0426: 1, H0529: 1, L0641: 1, L0794: 1, L0775: 1, L0806: 1, L0805: 1, L0776: 1, L0658: 1, H0520: 1 | S0010: 1, H0581: 1, H0012: 1, T0010: 1, H0290: 1, H0292: 1, H0615: 1, H0634: 1, H0560: 1, S0344: 1, L0521: 1, L0768: 1, L0791: 1, H0658: 1, H0134: 1, S0028: 1, L0753: 1, L0759: 1, L0591: 1, H0667: 1, H0136: 1, H0543: 1 and H0422: 1. | | | | |
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| | | | | | | | | | H0670: 1, S0330: 1, S0136: 1, H0521: 1, H0522: 1, H0555: 1, S0037: 1, S0206: 1, L0779: 1, L0759: 1, L0684: 1, S0192: 1 and S0412: 1. | | |
| 461 | HNFI54 | 919034 | 874 | 1 - 726 | 1774 | Gly-1 to Gly-20, Phe-27 to Val-34, Thr-70 to Lys-75, Pro-95 to Ala-101, Ile-162 to Arg-172. | | | AR061: 1, AR089: 1 H0305: 4, S0028: 3, H0589: 1, S0045: 1, H0416: 1, H0576: 1 and S0390: 1. | | |
| 462 | HSDF02 | 920435 | 472 | 2 - 376 | 1372 | Val-6 to Met-12. | | | AR061: 26, AR089: 21 S0031: 2 and S0044: 1. | | |
| 463 | HE8NS06 | 921076 | 473 | 3 - 1100 | 1373 | Gln-10 to Arg-15, Tyr-31 to Ser-45, Asn-59 to Thr-67, Glu-74 to Arg-79, Ser-137 to Lys-144, Pro-162 to Glu-167, Ser-213 to Gly-221, Ile-261 to Lys-267. | | | AR089: 3, AR061: 3 L0748: 9, H0013: 1, S0346: 1, H0090: 1, H0591: 1 and L0600: 1. | | |
| 464 | HASBA77 | 921365 | 474 | 45 - 467 | 1374 | Glu-3 to Ser-13, Asp-74 to Glu-79, Ala-92 to Ser-97, | | | AR050: 61, AR054: 60, AR051: 49, AR089: 9, AR061: 2 | | |

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| | | | | | | His-114 to Ala-125. | L0804: 3, L0748: 3, L0749: 3, S0196: 3, H0530: 2, H0413: 2, L0777: 2, H0686: 1, S0114: 1, H0341: 1, H0638: 1, H0393: 1, H0175: 1, H0071: 1, H0321: 1, H0561: 1, L0769: 1, L0794: 1, L0803: 1, L0805: 1, L0790: 1, L0740: 1, L0747: 1, L0758: 1, S0260: 1 and H0543: 1. | | | |
| 465 | HSKDP26 | 921366 | 875 | 61 - 588 | 1775 | Asp-66 to Glu-71, Ala-84 to Ser-89, His-106 to Ala-118, Tyr-130 to Leu-164, Leu-168 to Val-175. | AR089: 2, AR061: 2 T0074: 3, H0014: 1, S0027: 1 and S0028: 1. | | | |
| 466 | HMTAY52 | 921948 | 476 | 107 - 892 | 1376 | Gln-8 to Ser-16. | AR089: 4, AR061: 2 L0748: 4, L0758: 4, H0457: 3, L0754: 3, S0418: 2, H0253: 2, H0052: 2, S0116: 1, S0356: 1, S0278: 1, H0261: 1, S0222: 1, H0370: 1, H0486: 1, T0082: 1, S0474: 1, | | | |

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| 467 | HSDJG01 | 922453 | 477 | 100 - 789 | 1377 | Asp-18 to Leu-23, Asp-29 to Phe-34, His-45 to Asn-52, Gln-64 to Tyr-70, Thr-125 to Arg-131, Glu-133 to His-140, Glu-187 to Ile-195, Asn-224 to Phe-229. | H0057: 1, S0050: 1, H0594: 1, H0213: 1, H0553: 1, H0628: 1, H0617: 1, H0040: 1, H0100: 1, H0494: 1, H0207: 1, H0633: 1, L0763: 1, L0770: 1, L0769: 1, L0796: 1, L0642: 1, L0806: 1, L0805: 1, L0789: 1, L0665: 1, S0052: 1, H0144: 1, H0539: 1, H0518: 1, S0152: 1, L0749: 1, L0750: 1, L0777: 1, L0752: 1, L0601: 1, S0192: 1, S0194: 1 and H0506: 1. | | | |
| 468 | HHEPF30 | 928000 | 478 | 1 - 588 | 1378 | Gly-4 to Gln-10. | AR089: 2, AR061: 2 H0647: 1, H0435: 1, H0518: 1, H0521: 1, S0260: 1 and L0603: 1. | AR089: 15, AR061: 7 L0803: 7, L0759: 6, S0358: 4, L0748: 4, L0754: 4, L0749: 4, L0662: 3, H0413: 2, | 15q | |

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| 469 | HTLAB16 | 929948 | 479 | 1 - 960 | 1379 | | | H0529: 2, L0805: 2, H0672: 2, L0758: 2, S0040: 1, L0005: 1, S0360: 1, S0045: 1, H0581: 1, H0015: 1, H0083: 1, S0003: 1, L0142: 1, H0628: 1, H0090: 1, L0769: 1, L0667: 1, L0771: 1, L0790: 1, H0693: 1, H0519: 1, S0378: 1, L0745: 1, L0747: 1, L0777: 1, L0755: 1, L0731: 1, L0485: 1, S0026: 1, H0667: 1, S0242: 1, S0196: 1 and H0543: 1. | | |
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| 470 | HOHCW42 | 930431 | 480 | 2719 - 1634 | 1380 | Glu-12 to Arg-29, Gly-62 to Phe-69. | AR089: 0, AR061: 0 H0255: 4, H0254: 1, H0638: 1, H0587: 1, S0250: 1, H0617: 1, H0547: 1, H0519: 1, S0032: 1, L0591: 1, H0665: 1 and H0216: 1. | | |
| 471 | HCHNX75 | 931615 | 481 | 1 - 720 | 1381 | | AR089: 2, AR061: 2 L0794: 6, L0758: 6, H0599: 4, L0748: 4, L0759: 4, H0620: 3, L0806: 3, L0809: 3, H0547: 3, L0750: 3, L0752: 3, L0731: 3, H0624: 2, H0484: 2, H0549: 2, H0497: 2, H0486: 2, H0052: 2, H0150: 2, L0471: 2, H0181: 2, S0002: 2, H0529: 2, L0517: 2, L0666: 2, H0520: 2, L0757: 2, S0116: 1, S0045: 1, S0278: 1, H0013: 1, L0738: 1, H0050: 1, H0012: 1, H0622: 1, T0023: 1, H0087: 1, T0067: 1, H0494: 1, S0142: 1, S0344: 1, L0763: 1, L0769: 1, L0768: 1, | | |

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| 472 | HBCBA92 | 933093 | 482 | 1342 - 374 | 1382 | Ser-82 to Gly-87. | L0803: 1, L0650: 1, L0775: 1, L0805: 1, L0776: 1, L0655: 1, L0657: 1, L0658: 1, L0636: 1, L0384: 1, S0052: 1, H0144: 1, S0374: 1, H0519: 1, S0328: 1, H0696: 1, L0439: 1, L0751: 1, L0754: 1 and L0753: 1. | | |
| | | | | | | AR061: 10, AR089: 6 H0370: 13, H0620: 7, H0556: 4, L0794: 4, L0617: 3, H0251: 3, H0144: 3, L0438: 3, L0439: 3, L0752: 3, H0265: 2, S0358: 2, S0278: 2, H0486: 2, T0042: 2, S0210: 2, L0518: 2, L0666: 2, H0684: 2, H0134: 2, H0555: 2, L0743: 2, T0002: 1, S0134: 1, S0116: 1, H0484: 1, S0420: 1, H0208: 1, H0052: 1, H0012: 1, S0050: 1, H0015: 1, H0594: 1, S6028: 1, H0031: 1, H0598: 1, H0634: 1, H0264: 1. | | | |

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| | | | | | | | | | H0100: 1, S0464: 1, S0142: 1, L0640: 1, L0763: 1, L0773: 1, L0662: 1, L0768: 1, L0807: 1, L0382: 1, L0789: 1, H0519: 1, S0330: 1, S3014: 1, L0747: 1, L0758: 1, H0216: 1, H0542: 1 and H0543: 1. | | | |
| 473 | HHEJJE1 | 933110 | 483 | 3 - 608 | 1383 | Arg-11 to Arg-16, Gln-34 to Arg-40, Ser-119 to Gln-126, Lys-147 to Gly-157. | | | AR061: 7, AR089: 4 L0777: 8, H0046: 3, H0263: 2, L0803: 2, L0804: 2, S0360: 1, S0045: 1, H0619: 1, H0642: 1, H0013: 1, H0244: 1, H0039: 1, H0591: 1, L0641: 1, L0766: 1, L0517: 1, H0539: 1 and L0779: 1. | | | |
| 474 | HTXNN68 | 933670 | 484 | 1 - 960 | 1384 | Glu-9 to Gly-14, Pro-28 to Cys-35. | | | AR061: 5, AR089: 2 H0556: 2, L0770: 2, H0395: 1, S0040: 1, H0657: 1, H0194: 1, H0024: 1, L0667: 1, L0766: 1, H0521: 1, L0740: 1, L0779: 1 and L0588: 1. | | | |
| 475 | HWFW06 | 933671 | 485 | 3 - 533 | 1385 | | | | AR089: 13, AR061: 6 H0556: 2, L0770: 2, | | | |

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| | | | | | | | | H0395: 1, S0040: 1, H0657: 1, H0194: 1, H0024: 1, L0667: 1, L0766: 1, H0521: 1, L0740: 1, L0779: 1 and L0588: 1. | | | |
| 476 | HE2SY77 | 934771 | 486 | 3 - 338 | 1386 | | Gln-21 to Trp-32, Lys-81 to Leu-86, Pro-100 to Cys-107. | AR089: 1, AR061: 0 H0624: 1 and S0028: 1. | | | |
| 477 | HSHCO49 | 934819 | 487 | 113 - 766 | 1387 | | Ser-1 to Thr-7, Asp-41 to Cys-50, Glu-53 to Gly-61, Asn-89 to Glu-96, Glu-113 to Gln-119. | AR061: 10, AR089: 10 H0519: 1 and S0037: 1. | | | |
| 478 | HMUBI13 | 937820 | 488 | 237 - 899 | 1388 | | Phe-10 to Lys-15, Glu-108 to Gly-113, Pro-133 to Lys-142, Glu-152 to Thr-159, Val-196 to Glu-201, Val-216 to Tyr-221. | AR089: 17, AR061: 2 H0521: 5, L0759: 4, S0358: 3, L0757: 3, S0046: 2, H0494: 2, L0662: 2, L0740: 2, H0663: 1, H0638: 1, S0132: 1, H0549: 1, H0586: 1, H0590: 1, H0024: 1, H0083: 1, H0252: 1, H0591: 1, H0551: 1, H0059: 1, H0529: 1, L0389: 1, L0775: 1, L0776: 1, L0665: 1, L0438: 1, H0547: 1, H0435: 1, S0037: 1, L0439: 1, | | | |

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| 479 | HBXGL55 | 938766 | 489 | 777 - 1952 | 1389 | <p>Leu-15 to Leu-24, Pro-42 to Asp-54, Ala-123 to Gln-139, Leu-143 to Ala-148, Arg-165 to Asp-170, Arg-176 to Ser-183, Gly-211 to Thr-230, Ser-259 to Asp-268, Gly-309 to Gly-319, Val-326 to Ile-341, Pro-359 to Phe-373, Asp-382 to Asp-392.</p> | <p>L0755: 1, S0434: 1, L0596: 1, L0604: 1, H0667: 1, H0543: 1 and H0422: 1.</p> <p>AR089: 1, AR061: 1 L0769: 8, L0766: 7, L0771: 6, L0806: 6, H0253: 5, H0135: 4, L0741: 4, L0750: 4, H0295: 3, L0774: 3, L0805: 3, L0439: 3, L0751: 3, L0777: 3, L0755: 3, L0731: 3, H0392: 2, L0471: 2, L0770: 2, L0761: 2, L0740: 2, H0624: 1, H0583: 1, H0484: 1, L0617: 1, S0045: 1, S0278: 1, H0438: 1, H0013: 1, H0706: 1, H0618: 1, H0581: 1, H0544: 1, H0046: 1, H0024: 1, T0010: 1, H0286: 1, H0428: 1, H0622: 1, H0124: 1, H0634: 1, H0264: 1, T0042: 1, L0763: 1, L0800: 1, L0794: 1, L0803: 1, L0804: 1, L0650: 1, L0775: 1,</p> | | |
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| | | | | | | | | L0659: 1, L0636: 1, L0783: 1, L0789: 1, S0126: 1, H0522: 1, L0779: 1, L0752: 1, L0753: 1 and L0604: 1. | | | |
| 480 | HAFAH26 | 940254 | 490 | 1 - 1053 | 1390 | | | AR061: 5, AR089: 2 H0643: 2, L0803: 2, S0452: 2, T0049: 1, H0580: 1, H0013: 1, H0156: 1, H0581: 1, H0179: 1, H0271: 1, H0040: 1, S0422: 1, L0369: 1, L0766: 1, L0655: 1, L0607: 1, L0791: 1, H0693: 1, H0670: 1, S0380: 1, H0579: 1, L0777: 1, L0752: 1, S0011: 1 and H0653: 1. | | | |
| 481 | HARMG23 | 942860 | 491 | 1 - 612 | 1391 | Thr-4 to Ser-12. | | AR061: 1, AR089: 1 L0777: 3, L0769: 2, S0132: 1, H0592: 1, H0586: 1, H0492: 1, H0004: 1, H0041: 1, H0606: 1, H0038: 1, H0264: 1, S0002: 1, L0371: 1, L0761: 1, L0646: 1, L0794: 1, L0766: 1, L0774: 1, L0664: 1, L0748: 1, | | | |

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| | | | | | | | | | L0751: 1, L0750: 1 and L0779: 1. | | |
| 482 | HO8MV44 | 943224 | 492 | 2 - 1138 | 1392 | Val-18 to Lys-23, Arg-158 to Trp-167, Ser-176 to Ser-185, Gly-200 to Tyr-207, Pro-216 to Trp-221, Val-257 to Ser-266, Ile-304 to Val-316, Pro-319 to Thr-325, Thr-350 to Ser-358. | | | AR061: 2, AR089: 2 L0766: 2, L0740: 2, S0356: 1, H0415: 1, H0598: 1, L0803: 1, L0774: 1, L0518: 1, H0539: 1, L0749: 1, L0779: 1 and L0777: 1. | | |
| 483 | HE9CJ28 | 949245 | 493 | 1506 - 145 | 1393 | Tyr-22 to Gly-40, Glu-56 to Glu-66. | | | AR061: 1, AR089: 1 H0619: 1, H0549: 1, H0486: 1, H0051: 1, S0250: 1, H0561: 1, S0428: 1, H0144: 1, H0539: 1, L0731: 1, L0592: 1, L0366: 1 and H0667: 1. | | |
| 484 | HE8AZ89 | 950713 | 494 | 2 - 667 | 1394 | | | | AR089: 1, AR061: 0 H0624: 1, H0013: 1, L0471: 1, S0250: 1, H0038: 1, H0100: 1, T0042: 1, S0150: 1, L0438: 1 and L0592: 1. | | |
| 485 | HF8KW94 | 950717 | 495 | 190 - 1047 | 1395 | Arg-1 to Gly-6, Thr-74 to Ser-79, Pro-88 to Arg-96. | | | AR054: 1, AR050: 1, AR089: 1, AR061: 1 S0028: 3, S0222: 2, L0105: 2, S0050: 2, S0390: 2, S0260: 2, | | |

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| 486 | HISAF41 | 951370 | 496 | 1681 - 1226 | 1396 | | | | H0344: 1, H0381: 1, S0282: 1, H0618: 1, S0051: 1, S6028: 1, H0271: 1, H0383: 1, H0264: 1 and S0038: 1. AR061: 1, AR089: 1 L0439: 5, H0529: 3, L0759: 3, S0360: 2, H0024: 2, L0766: 2, L0804: 2, L0779: 2, L0362: 2, H0556: 1, H0656: 1, H0575: 1, H0544: 1, H0015: 1, H0616: 1, H0551: 1, H0412: 1, H0413: 1, L0770: 1, L0662: 1, L0803: 1, L0805: 1, L0655: 1, L0659: 1, L0790: 1, L0665: 1, H0547: 1, H0658: 1, H0539: 1, H0521: 1, L0740: 1, L0745: 1, L0777: 1, L0755: 1, H0445: 1, S0026: 1, H0665: 1 and S0242: 1. | | |
| 487 | HDPJH11 | 951371 | 497 | 1 - 519 | 1397 | Phe-22 to Thr-27, Lys-71 to Arg-76, Ile-96 to Gly-102, Pro-121 to Trp-133. | | | AR061: 1, AR089: 1 L0439: 5, H0529: 3, L0759: 3, S0360: 2, H0024: 2, L0766: 2, L0804: 2, L0779: 2, | | |

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| 488 | HLHCP93 | 950792 | 498 | 460 - 218 | 1398 | Lys-18 to Ile-23. | L0362: 2, H0556: 1, H0656: 1, H0575: 1, H0544: 1, H0015: 1, H0616: 1, H0551: 1, H0412: 1, H0413: 1, L0770: 1, L0662: 1, L0803: 1, L0805: 1, L0655: 1, L0659: 1, L0790: 1, L0665: 1, H0547: 1, H0658: 1, H0539: 1, H0521: 1, L0740: 1, L0745: 1, L0777: 1, L0755: 1, H0445: 1, S0026: 1, H0665: 1 and S0242: 1. AR061: 2, AR089: 1 L0439: 5, H0529: 3, L0759: 3, S0360: 2, H0024: 2, L0766: 2, L0803: 2, L0804: 2, L0779: 2, L0362: 2, H0556: 1, H0656: 1, H0575: 1, H0544: 1, H0015: 1, H0616: 1, H0551: 1, H0412: 1, H0413: 1, L0770: 1, L0662: 1, L0805: 1, L0655: 1, L0659: 1, L0790: 1, L0665: 1, H0547: 1, H0658: 1, | | |
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| 489 | HAIBC14 | 951372 951671 | 876 499 | 175 - 717 215 - 796 | 1776 1399 | Lys-10 to Gln-20. | AR089: 3, AR061: 3 L0766: 8, L0803: 8, H0046: 7, L0740: 7, L0752: 7, L0754: 6, H0318: 5, H0038: 5, H0551: 5, L0659: 5, S0152: 5, H0624: 4, L0471: 4, S0003: 4, L0666: 4, L0747: 4, L0756: 4, H0422: 4, H0556: 3, S0360: 3, S0045: 3, H0586: 3, H0486: 3, H0590: 3, H0581: 3, H0628: 3, L0662: 3, L0794: 3, L0657: 3, L0809: 3, L0790: 3, L0663: 3, L0664: 3, L0665: 3, H0520: 3, H0658: 3, L0439: 3, L0779: 3, L0777: 3, S0026: 3, H0265: 2, H0657: 2, S0212: 2, H0661: 2, S0418: 2 S0376: 2 | AR089: 3, AR061: 3 L0766: 8, L0803: 8, H0046: 7, L0740: 7, L0752: 7, L0754: 6, H0318: 5, H0038: 5, H0551: 5, L0659: 5, S0152: 5, H0624: 4, L0471: 4, S0003: 4, L0666: 4, L0747: 4, L0756: 4, H0422: 4, H0556: 3, S0360: 3, S0045: 3, H0586: 3, H0486: 3, H0590: 3, H0581: 3, H0628: 3, L0662: 3, L0794: 3, L0657: 3, L0809: 3, L0790: 3, L0663: 3, L0664: 3, L0665: 3, H0520: 3, H0658: 3, L0439: 3, L0779: 3, L0777: 3, S0026: 3, H0265: 2, H0657: 2, S0212: 2, H0661: 2, S0418: 2 S0376: 2 | 10p15 | 147730 |
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| | | H0014: 2, H0266: 2, S0214: 2, H0032: 2, H0068: 2, H0163: 2, H0040: 2, L0598: 2, L0520: 2, L0646: 2, L0771: 2, L0805: 2, L0776: 2, L0655: 2, H0519: 2, H0689: 2, H0660: 2, H0648: 2, H0478: 2, L0731: 2, L0758: 2, H0445: 2, L0595: 2, L0601: 2, S0242: 2, S0040: 1, S0402: 1, S0134: 1, S0116: 1, H0341: 1, H0638: 1, S0354: 1, S0408: 1, S0132: 1, H0619: 1, S0278: 1, H0550: 1, S0222: 1, H0431: 1, H0601: 1, H0587: 1, H0250: 1, L0021: 1, H0575: 1, H0251: 1, H0596: 1, T0110: 1, H0150: 1, H0123: 1, H0050: 1, H0267: 1, S0250: 1, H0328: 1, H0615: 1, H0428: 1, L0483: 1, H0553: 1, H0169: 1, S0036: 1, H0090: 1, H0591: 1, H0616: 1, | |
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| 491 | HWADY95 | 951731 | 501 | 2 - 514 | 1401 | Arg-15 to Asp-21, Arg-59 to Gly-66, Ile-69 to Glu-74, Lys-82 to Tyr-87, Met-95 to Asp-100, Lys-163 to Arg-171. | Phe-114 to Lys-126, Asn-198 to Ser-203, Asn-234 to Ile-242, Glu-264 to Pro-270. | H0494: 1 and S0440: 1. | | |
| 492 | HCHAG27 | 952058 | 502 | 3 - 812 | 1402 | Ser-50 to Pro-62, Ala-112 to Ser-125. | | AR089: 11, AR061: 3 L0748: 3, H0549: 2, H0144: 2, L0021: 1, H0618: 1, H0318: 1, H0581: 1, H0239: 1, H0510: 1, H0264: 1, L0779: 1, L0758: 1, L0596: 1 and S0106: 1. | | |
| 493 | HPCRA07 | 952124 | 503 | 701 - 15 | 1403 | Glv-27 to Glv-38. | | AR089: 3, AR061: 1 L0517: 6, L0751: 6, H0370: 4, L0764: 3, L0666: 3, S0007: 2, L0769: 2, L0646: 2, L0664: 2, H0520: 2, H0484: 1, H0483: 1, S0046: 1, H0644: 1, S0036: 1, H0494: 1, S0440: 1, H0538: 1, L0770: 1, L0772: 1, L0773: 1, L0803: 1, L0657: 1, L0659: 1, L0809: 1, H0690: 1, H0684: 1, H0660: 1, H0627: 1, S0027: 1, L0755: 1 and H0707: 1. | | |

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| 494 | HDMAF23 | 952729 | 504 | 1283 - 219 | 1404 | Arg-6 to Glu-12, Tyr-30 to Thr-35, Val-42 to His-52. | Thr-67 to Arg-72, Val-87 to Ser-98, Glu-170 to Gly-176, Lys-190 to Asp-200. | AR089: 6, AR061: 3 S0026: 2, H0638: 1, H0486: 1, H0318: 1, S0214: 1, H0090: 1, T0041: 1, H0494: 1, L0520: 1, L0646: 1, L0666: 1, H0144: 1, S0374: 1, S0146: 1, L0750: 1 and L0485: 1. | | |
| 495 | HRGBU12 | 952730 | 505 | 3 - 473 | 1405 | Ala-1 to Ser-7, Gln-31 to Leu-46, Arg-49 to Glu-55, Tyr-73 to Asp-79. | Ala-1 to Ser-7, Gln-31 to Leu-46, Arg-49 to Glu-55, Tyr-73 to Asp-79. | AR061: 3, AR089: 3 H0656: 1, H0038: 1, S0210: 1, H0134: 1, H0445: 1 and L0485: 1. | | |
| 496 | HADF082 | 953295 | 506 | 16 - 1005 | 1406 | Ala-8 to Pro-23, Ala-25 to Pro-30, Arg-46 to Glu-53. | Ala-8 to Pro-23, Ala-25 to Pro-30, Arg-46 to Glu-53. | AR089: 1, AR061: 1 L0766: 7, L0756: 5, H0521: 3, L0777: 3, S0007: 2, H0413: 2, L0761: 2, L0771: 2, L0666: 2, L0748: 2, L0751: 2, H0306: 1, H0402: 1, S0354: 1, S0278: 1, H0441: 1, H0455: 1, H0587: 1, H0486: 1, H0427: 1, H0599: 1, H0581: 1, H0052: 1, H0009: 1. | | |

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| 497 | HCGAF54 | 954048 | 507 | 1 - 636 | 1407 | | | | H0024: 1, H0617: 1, H0040: 1, L0763: 1, L0769: 1, L0646: 1, L0650: 1, L0774: 1, L0775: 1, L0651: 1, L0806: 1, L0655: 1, L0659: 1, L0663: 1, L0665: 1, H0593: 1, H0684: 1, H0436: 1, L0754: 1, L0747: 1, L0758: 1, L0366: 1 and H0543: 1. | | |
| | | | | | | | | | AR089: 15, AR061: 7 L0747: 6, L0749: 6, L0766: 5, L0775: 5, H0547: 5, L0758: 4, S0358: 3, H0031: 3, L0744: 3, L0759: 3, S0046: 2, L0471: 2, H0616: 2, T0042: 2, L0764: 2, L0774: 2, L0659: 2, L0748: 2, L0740: 2, L0756: 2, L0779: 2, H0668: 2, H0624: 1, H0556: 1, H0661: 1, H0449: 1, H0125: 1, H0351: 1, H0614: 1, H0455: 1, H0438: 1, H0632: 1, H0486: 1, H0590: 1. | | |

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| | | | | | | Glu-204 to Gly-214. | | | |
| | | | 877 | 2180 - 1323 | 1777 | Leu-29 to Arg-34, Glu-45 to Thr-50, Tyr-67 to Arg-73, Pro-83 to Gln-108, Asp-117 to Val-123, Gln-148 to Glu-155. | | | |
| 499 | HWWCL36 | 955759 | 509 | 2 - 676 | 1409 | | | | AR089: 7, AR061: 2 H0657: 1, T0023: 1, L0803: 1, H0521: 1, L0731: 1, S0026: 1 and H0423: 1. |
| 500 | HDTEN41 | 955895 | 510 | 1 - 1464 | 1410 | Pro-1 to Arg-16. | | | AR089: 17, AR061: 7 19 |
| 501 | HSDDDD20 | 956046 | 511 | 1 - 657 | 1411 | Asp-25 to Glu-38, Ala-98 to Phe-104, Gln-152 to Leu-157. | | | AR089: 1, AR061: 0 S0028: 3, S0001: 2, H0617: 2, L0361: 2, S0356: 1, S0045: 1, H0619: 1, S0278: 1, H0250: 1, H0231: 1, H0181: 1, S0390: 1 and S0031: 1. |
| 502 | HDPBL08 | 959377 | 512 | 173 - 979 | 1412 | | | | AR061: 2, AR089: 2 H0616: 4, L0758: 4, H0341: 2, S0358: 2, L0438: 2, L0748: 2, L0779: 2, H0265: 1, S0222: 1, H0431: 1, H0013: 1, H0253: 1, S0010: 1, H0428: 1. |

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| | | | | | | | | | L0456: 1, H0038: 1, L0151: 1, H0063: 1, H0494: 1, L0767: 1, L0657: 1, S0052: 1, S0152: 1, H0521: 1, L0750: 1, H0707: 1 and H0542: 1. | | |
| 503 | HMELJ75 | 960354 | 513 | 114 - 1187 | 1413 | Leu-16 to Phe-21, Thr-69 to Lys-74, Asn-87 to His-92, Thr-126 to Leu-137, Phe-154 to Lys-164, Ala-171 to Asp-178, Ile-192 to Thr-203, Glu-261 to Ser-273. | | | AR061: 4, AR089: 3 S0003: 2, H0591: 2, H0529: 2, L0663: 2, L0750: 2, L0752: 2, L0596: 2, H0171: 1, H0341: 1, H0662: 1, S0420: 1, S0132: 1, H0411: 1, S0222: 1, H0013: 1, H0266: 1, H0428: 1, H0039: 1, H0622: 1, L0483: 1, H0644: 1, H0598: 1, H0040: 1, H0634: 1, L0564: 1, H0280: 1, S0150: 1, L0800: 1, L0764: 1, L0662: 1, L0766: 1, L0529: 1, L0666: 1, H0144: 1, H0660: 1, S0152: 1, H0521: 1, L0779: 1, L0777: 1, L0757: 1, L0758: 1 and H0543: 1. | | |
| 504 | HLTCU08 | 960951 | 514 | 27 - 686 | 1414 | Thr-1 to Asn-17, | | | AR061: 4, AR089: 3 | | |

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| Lys-38 to Glu-45, Tyr-74 to Arg-79, Ala-90 to Val-95, Phe-124 to Gln-142, Val-180 to His-189. | L0777: 13, L0740: 8, L0759: 5, L0608: 5, H0031: 4, H0042: 3, L0771: 3, L0665: 3, L0748: 3, L0439: 3, L0754: 3, H0024: 2, L0769: 2, L0794: 2, L0766: 2, L0806: 2, L0790: 2, H0521: 2, L0750: 2, L0756: 2, L0758: 2, L0592: 2, H0556: 1, H0159: 1, T0049: 1, H0657: 1, S0007: 1, S0046: 1, H0619: 1, S0222: 1, H0574: 1, H0486: 1, S0346: 1, H0318: 1, H0581: 1, H0052: 1, H0327: 1, H0051: 1, T0010: 1, H0039: 1, L0483: 1, L0143: 1, H0032: 1, H0673: 1, H0090: 1, H0038: 1, T0067: 1, S0038: 1, H0529: 1, L0640: 1, L0763: 1, L0639: 1, L0667: 1, L0764: 1, L0662: 1, L0768: 1, L0523: 1, L0657: 1, L0659: 1, H0144: 1, H0659: 1, H0658: 1. |
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| | | | | | | | | | S0328: 1, H0539: 1, S0378: 1, S0028: 1, L0747: 1, L0752: 1, L0753: 1, L0755: 1, L0731: 1, L0596: 1, L0595: 1, H0543: 1 and S0412: 1. | | | |
| 505 | HTOHK41 | 960955 | 515 | 1065 - 151 | 1415 | His-10 to Pro-16. | | | AR089: 20, AR061: 6 H0265: 2, S0040: 1, H0250: 1 and H0264: 1. | | | |
| 506 | HTKAA03 | 961002 | 516 | 2 - 202 | 1416 | Asn-1 to Thr-9, Thr-40 to Asp-51. | | | S0300: 1, S0028: 1 and T0047: 1. | | | |
| 507 | HMSGF27 | 962420 | 517 | 3 - 332 | 1417 | Arg-1 to Asp-6, Ala-47 to Pro-58. | | | AR089: 12, AR061: 8 L0766: 4, H0052: 3, L0662: 3, L0776: 3, L0666: 3, L0665: 3, H0521: 3, H0438: 2, H0581: 2, H0263: 2, H0494: 2, L0763: 2, L0770: 2, L0769: 2, L0649: 2, L0664: 2, L0748: 2, L0439: 2, L0747: 2, S0436: 2, H0265: 1, H0556: 1, S0040: 1, S0444: 1, S0278: 1, H0415: 1, H0403: 1, H0643: 1, S0280: 1, H0575: 1, H0194: 1, H0309: 1, H0545: 1 H0046: 1 | | | |

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| 508 | HHFLM17 | 963511 | 518 | 3 - 470 | 1418 | Pro-45 to Pro-52, Asn-79 to Ala-84, Gly-124 to Ser-129. | AR089: 2, AR061: 1 H0619: 1, H0529: 1, L0375: 1 and H0543: 1. | L0157: 1, H0375: 1, L0483: 1, H0553: 1, H0412: 1, H0646: 1, S0002: 1, L0796: 1, L0644: 1, L0764: 1, L0774: 1, L0376: 1, L0806: 1, L0654: 1, L0659: 1, L0383: 1, S0126: 1, H0684: 1, H0435: 1, H0478: 1, S0028: 1, L0751: 1, L0754: 1, L0749: 1, L0750: 1, L0779: 1, L0759: 1, H0543: 1 and H0423: 1. | 1p32-p34 | 120950, 120960, 130500, 133200, 138140, 168360, 171760, 171760, 176100, 176100, 178300, 187040, 230000, 255800, 600101, |
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| | | | | | | | | | 600650, 600650, 600722, 600722 |
| 509 | HLICLI0 | 964035 | 519 | 3 - 761 | 1419 | Glu-121 to Lys-126, Pro-148 to Lys-154, Thr-181 to Asp-187, Val-208 to Asp-214, Pro-223 to Phe-231, Glu-239 to Lys-245. | | AR089: 99, AR061: 59 H0393: 1, S0278: 1, H0643: 1, H0196: 1, H0231: 1, H0200: 1, H0355: 1, S0037: 1, S0027: 1, H0445: 1 and H0423: 1. | |
| 510 | HCUAZ04 | 965585 | 520 | 546 - 214 | 1420 | Lys-6 to Phe-11. | | AR089: 1, AR061: 0 L0769: 8, L0748: 4, L0759: 4, H0038: 3, L0750: 3, L0755: 3, H0556: 2, S0356: 2, H0574: 2, L0163: 2, L0766: 2, L0776: 2, L0663: 2, L0752: 2, L0731: 2, L0599: 2, H0255: 1, H0306: 1, H0125: 1, S0376: 1, H0580: 1, H0455: 1, H0497: 1, H0331: 1, L0021: 1, H0004: 1, H0618: 1, S0010: 1, H0546: 1, H0545: 1, H0123: 1, H0081: 1, H0578: 1, H0051: 1, H0510: 1, H0188: 1, | |

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| 513 | HLICJ19 | 966969 | 523 | 1 - 321 | 1423 | 1778 | Glu-14 to Glu-24, Glu-38 to Ser-62, Ala-177 to Ala-198, Glu-235 to Arg-240, His-257 to Lys-374. | H0658: 1, H0660: 1, H0521: 1, H0555: 1, S0028: 1, L0742: 1, L0756: 1, S0192: 1, S0242: 1, S0194: 1 and S0276: 1. | | |
| 514 | HDPSM18 | 967483 | 524 | 1 - 315 | 1424 | 1424 | Thr-27 to Asn-33. | AR061: 27, AR089: 6 S0040: 1, H0355: 1, H0328: 1, L0374: 1, L0794: 1, L0766: 1 and S3014: 1. | | |
| 515 | HMAKJ82 | 967593 | 525 | 1 - 501 | 1425 | 1425 | Thr-3 to Gly-13, Trp-35 to Glu-40, Ser-51 to His-56. | AR061: 2, AR089: 1 H0556: 1, S0212: 1, H0373: 1, H0553: 1, H0063: 1, H0477: 1, S0152: 1, H0521: 1 and S0026: 1. | | |

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| 516 | HFPIX37 | 971428 | 526 | 1 - 507 | 1426 | Pro-75 to Asp-84, Pro-92 to Pro-101, Arg-161 to Trp-167. | H0549: 2, H0497: 2, H0486: 2, H0052: 2, H0150: 2, L0471: 2, H0181: 2, S0002: 2, H0529: 2, L0517: 2, L0666: 2, H0520: 2, L0757: 2, S0116: 1, S0045: 1, S0278: 1, H0013: 1, L0738: 1, H0050: 1, H0012: 1, H0622: 1, T0023: 1, H0087: 1, T0067: 1, H0494: 1, S0142: 1, S0344: 1, L0763: 1, L0769: 1, L0768: 1, L0803: 1, L0650: 1, L0775: 1, L0805: 1, L0776: 1, L0655: 1, L0657: 1, L0658: 1, L0636: 1, L0384: 1, S0052: 1, H0144: 1, S0374: 1, H0519: 1, S0328: 1, H0696: 1, L0439: 1, L0751: 1, L0754: 1 and L0753: 1. AR089: 4, AR061: 1 H0583: 1, H0662: 1, S0222: 1, S0049: 1, H0272: 1, H0670: 1, H0521: 1, H0555: 1 and | | |
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| 517 | HHEKP47 | 974402 | 527 | 75 - 527 | 1427 | Ser-1 to Thr-7, Pro-15 to Asp-22, Glu-138 to Ser-143. | S0436: 1. AR089: 1, AR061: 1 H0542: 6, H0637: 3, H0580: 3, H0555: 2, H0592: 1, H0586: 1, H0544: 1, H0546: 1, H0545: 1, H0529: 1, H0703: 1, H0593: 1, H0521: 1 and H0543: 1. | 1q32 | 114208, 114208, 119300, 120620, 120620, 120920, 134370, 134370, 134370, 134580, 145260, 150310, 150310, 179820, 191045, 600105, 600759, 601494, 601975 |
| 518 | HTPDV62 | 418671 | 528 | 2 - 358 | 1428 | | AR061: 7, AR089: 4 H0663: 2, H0069: 2, H0634: 2, H0635: 1, H0618: 1 and H0039: 1. | 1q32-q41 | 114208, 114208, 119300, 120620, 120620, 120920, 134370, 134370, 134370, 134580, |

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| | | | | | | | | | | 145260, 150310, 150310, 179820, 191045, 276901, 600105, 600332, 600759, 601494, 601744, 601975 |
| 519 | HUSAJ73 | 567234 | 529 | 1 - 201 | 1429 | | | AR061: 8, AR089: 7 S0045: 1, S0046: 1, H0574: 1 and H0268: 1. | 5 | |
| 520 | HSKCJ76 | 747380 | 530 | 115 - 414 | 1430 | Phe-12 to Thr-17. | | AR061: 6, AR089: 5 | 5 | |
| 521 | HCEOX38 | 881200 | 531 | 3 - 386 | 1431 | Met-1 to Ile-23, Asp-85 to Asp-91. | | AR089: 2, AR061: 1 H0052: 1 and H0435: 1. | 17p13-p12 | 100710, 138190, 231200, 254210, 262850, 271900, 600179, 600977, 601202, 601777 |
| 522 | HFICR59 | 911317 | 532 | 2 - 721 | 1432 | Ser-2 to Lys-7, Thr-73 to Ala-86, Gly-108 to Asn-113. | | AR089: 1, AR061: 0 L0794: 6, L0598: 2, L0803: 2, L0748: 2. | | |

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| 523 | HPDVO67 | 911405 | 533 | 1 - 645 | 1433 | Ser-184 to Val-190. | S0040: 1, S0046: 1, H0431: 1, H0318: 1, L0766: 1, L0606: 1, L0749: 1, L0758: 1 and S0192: 1. | 19p13.3 | 108725, 120700, 133171, 136836, 145981, 147141, 164953, 188070, 600957, 601238, 601846, 602216, 602477 |
| | | | | | | Glu-1 to Asp-6, Thr-11 to Glu-20, Val-61 to Pro-67, Ala-128 to Leu-136, Glu-141 to Ser-147, Arg-173 to Pro-179. | AR089: 2, AR061: 2, L0751: 10, L0666: 4, L0743: 3, H0253: 2, H0622: 2, H0670: 2, L0779: 2, H0685: 1, H0181: 1, S0382: 1, L0372: 1, L0646: 1, L0773: 1, L0767: 1, L0768: 1, L0657: 1, L0665: 1, S0374: 1, H0658: 1, L0749: 1, L0777: 1, L0758: 1 and L0593: 1. | | |
| 524 | H2LAD53 | 952181 | 534 | 1 - 360 | 1434 | Glu-1 to Tyr-10, Lys-37 to Leu-44, Glu-66 to Leu-75, Glu-80 to His-91. | AR089: 18, AR061: 13, S0136: 47, L0769: 10, L0439: 7, L0750: 7, H0620: 5, L0776: 5, L0740: 5, L0752: 5, L0509: 4, L0809: 4, L0666: 4, L0748: 4, H0624: 3, H0265: 3, H0341: 3, S0418: 3, L0717: 3, L0764: 3, L0659: 3, L0755: 3, S0026: 3, H0556: 2, | | |

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| | S0356: 2, S0358: 2, S0360: 2, H0574: 2, T0060: 2, S0010: 2,, H0046: 2, H0510: 2, H0032: 2, H0169: 2, H0413: 2, H0646: 2, L0646: 2, L0766: 2, L0803: 2, L0805: 2, L0665: 2, S0374: 2, H0519: 2, H0659: 2, H0648: 2, S0328: 2, S0378: 2, S0380: 2, S3014: 2, L0756: 2, L0777: 2, L0731: 2, L0758: 2, L0588: 2, L0589: 2, L0594: 2, H0543: 2, H0171: 1, S0040: 1, T0049: 1, L0002: 1, H0657: 1, H0346: 1, H0255: 1, H0664: 1, H0305: 1, H0589: 1, S0376: 1, H0675: 1, S0045: 1, S0046: 1, H0586: 1, H0587: 1, H0333: 1, H0642: 1, H0331: 1, H0632: 1, H0486: 1, H0013: 1, H0427: 1, L0021: 1, H0575: 1, H0590: 1, S0182: 1, H0085: 1, H0596: 1, | | | | | | |
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| | H0546: 1, L0157: 1, H0572: 1, H0571: 1, H0024: 1, L0695: 1, H0373: 1, L0163: 1, S6028: 1, H0266: 1, S0003: 1, H0252: 1, T0006: 1, H0166: 1, H0674: 1, S0364: 1, L0455: 1, H0124: 1, H0598: 1, H0400: 1, H0135: 1, H0163: 1, H0038: 1, H0616: 1, H0551: 1, T0067: 1, H0100: 1, T0041: 1, S0448: 1, S0450: 1, H0509: 1, H0647: 1, S0208: 1, L0770: 1, L0637: 1, L0772: 1, L0372: 1, L0800: 1, L0374: 1, L0662: 1, L0388: 1, L0774: 1, L0775: 1, L0375: 1, L0653: 1, L0628: 1, L0513: 1, L0526: 1, L0518: 1, L0382: 1, L0663: 1, L0664: 1, L0565: 1, L0438: 1, H0660: 1, H0666: 1, S0044: 1, S0037: 1, S0206: 1, L0747: 1, L0780: 1, L0753: 1, |
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| | | | | | | | | L0757: 1, L0759: 1, H0445: 1, L0592: 1, L0485: 1, L0608: 1, L0603: 1, L0097: 1 and S0446: 1. | | |
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| 525 | HETLM90 | 972357 | 879 | 672 - 887 | 1779 | Glu-42 to Val-48, Glu-63 to Asp-72. | | AR061: 7, AR089: 6 S0404: 7, L0754: 4, L0731: 4, H0046: 3, L0662: 3, H0519: 2, L0439: 2, L0756: 2, L0758: 2, S0242: 2, H0171: 1, L0021: 1, H0194: 1, H0251: 1, L0471: 1, H0057: 1, S6028: 1, H0615: 1, H0063: 1, H0494: 1, L0598: 1, L0520: 1, L0646: 1, L0641: 1, L0794: 1, L0766: 1, L0803: 1, L0666: 1, H0144: 1, S0374: 1, H0690: 1, H0539: 1, S0380: 1, H0696: 1, H0436: 1, L0740: 1, L0755: 1 and S0031: 1. | | |
| 526 | HCBSE94 | 969287 | 536 | 270 - 410 | 1436 | Ser-1 to Gly-8, Lys-14 to Pro-21, | | AR089: 1 H0619: 5, L0439: 5, | | |

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| | | | Ser-25 to Cys-33, Pro-37 to Gly-44. | L0770: 4, T0049: 2, H0052: 2, H0544: 2, H0268: 2, L0748: 2, L0740: 2, L0749: 2, L0756: 2, L0759: 2, H0624: 1, H0170: 1, H0662: 1, H0306: 1, S0420: 1, S0376: 1, S0045: 1, S0132: 1, S0278: 1, H0587: 1, H0574: 1, S0280: 1, H0599: 1, H0546: 1, H0124: 1, H0135: 1, H0163: 1, H0551: 1, H0264: 1, H0269: 1, H0413: 1, H0646: 1, S0208: 1, L0631: 1, L0761: 1, L0764: 1, L0662: 1, L0766: 1, L0803: 1, L0806: 1, L0805: 1, L0653: 1, L0659: 1, L0809: 1, L0666: 1, L0665: 1, L0438: 1, H0670: 1, H0518: 1, H0436: 1, S0037: 1, S0027: 1, L0743: 1, L0750: 1, L0777: 1, L0758: 1, H0595: 1, L0601: 1, H0423: 1 and H0506: 1. |
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| | | 969299 | 881 | 889 - 1386 | 1781 | Pro-23 to Trp-28, Pro-35 to Lys-41, Gln-101 to Glu-110, Glu-122 to Gly-129. | | | |
| | | 971074 | 882 | 3 - 1097 | 1782 | | | | |
| 527 | HFXCU55 | 499457 | 537 | 183 - 1 | 1437 | Lys-32 to Lys-51. | AR061: 1, AR089: 0 S0001: 1 and H0150: 1. | | |
| 528 | HEPBV24 | 513261 | 538 | 73 - 393 | 1438 | Glu-24 to His-33. | AR089: 619, AR061: 539 S0001: 1 and H0150: 1. | | |
| 529 | HFRAU96 | 527840 | 539 | 13 - 363 | 1439 | | AR089: 1, AR061: 0 S0050: 1 and S0044: 1. | | |
| 530 | HTLBD23 | 527944 | 540 | 3 - 413 | 1440 | His-1 to Gly-6, Ser-13 to Phe-18. | AR061: 8, AR089: 3 H0013: 4, H0617: 2, S0428: 2, S0032: 2, S0001: 1, T0074: 1, H0253: 1, H0318: 1, S0050: 1, L0456: 1, H0268: 1 and S0390: 1. | | |
| 531 | HCEBM51 | 536558 | 541 | 3 - 470 | 1441 | Asp-17 to Ala-25. | AR089: 2, AR061: 1 H0040: 3, H0087: 3, H0052: 2, L0747: 2, L0601: 2, S0010: 1, H0327: 1, S0051: 1, H0181: 1, L0741: 1, L0745: 1, L0753: 1 and S0106: 1. | | |
| 532 | HSLFF79 | 609838 | 542 | 64 - 741 | 1442 | Phe-132 to Gln-137, Arg-209 to Gly-220. | AR089: 1, AR061: 0 S0028: 2 and S0300: 1. | | |
| | | 961693 | 883 | 866 - 174 | 1783 | Phe-137 to Gln-142, | | | |

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| 533 | HKTAB71 | 661483 | 543 | 3 - 398 | 1443 | Arg-214 to Gly-225. Asp-47 to Asn-53, Pro-118 to Thr-132. | AR089: 14, AR061: 4 L0774: 3, L0749: 2, H0239: 1, L0803: 1 and S0378: 1. | | | |
| 534 | HSDIF25 | 678003 | 544 | 36 - 446 | 1444 | | AR089: 1, AR061: 0 S0390: 1 and S0260: 1. | | | |
| 535 | HNHHW82 | 684342 | 545 | 3 - 284 | 1445 | Ala-1 to Arg-10, His-15 to Asp-20. | AR089: 11, AR061: 4 S0053: 2 and S0050: 1. | | | |
| 536 | HFATN41 | 712097 | 546 | 259 - 717 | 1446 | Gly-37 to Asp-50. | AR061: 3, AR089: 2 S0300: 1 and H0031: 1. | | | |
| 537 | HHEFFG80 | 733387 | 547 | 2 - 478 | 1447 | | AR089: 15, AR061: 6 H0050: 1 and H0522: 1. | | | |
| 538 | HSDEFF73 | 761657 | 548 | 3 - 515 | 1448 | | AR061: 139, AR089: 37 S0028: 1 and S0031: 1. | | | |
| 539 | HTLBH79 | 774422 | 549 | 3 - 572 | 1449 | | AR054: 22, AR051: 20, AR089: 4, AR061: 3, AR050: 2 L0439: 2, S0358: 1, H0486: 1, H0253: 1, H0593: 1 and H0522: 1. | | | |
| | | 797621 | 884 | 715 - 263 | 1784 | | | | | |
| | | 971837 | 885 | 307 - 828 | 1785 | Glu-11 to Arg-17. | | | | |
| 540 | HBWCD80 | 777346 | 550 | 2 - 868 | 1450 | Leu-26 to Ser-31, Pro-68 to Lys-82. | AR089: 1, AR061: 0 | | | |
| 541 | HSDKI89 | 786812 | 551 | 3 - 521 | 1451 | Asp-8 to Gly-26, Tyr-43 to Ser-49, Ser-137 to Lys-148. | AR061: 1, AR089: 1 | | | |

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| 542 | HIBDA29 | 810879 | 552 | 2 - 403 | 1452 | | AR089: 1, AR061: 1 T0010: 2, H0172: 1, H0100: 1, L0769: 1, L0792: 1, L0745: 1 and L0756: 1. | | |
| 543 | HLDQU68 | 825558 | 553 | 1 - 429 | 1453 | Trp-10 to Gly-16, Asp-30 to Ala-39, Glu-72 to Ser-87, Asn-112 to Trp-124. | AR061: 9, AR089: 2 H0351: 1 and H0510: 1. | | |
| 544 | HMUAS41 | 827510 | 554 | 2 - 385 | 1454 | Asn-37 to Gln-42, Thr-56 to Leu-62, Asn-68 to Lys-74. | AR089: 4, AR061: 2 S0007: 3, S0354: 2, H0529: 2, H0645: 1, H0052: 1 and H0039: 1. | | |
| 545 | HTXOH20 | 837509 | 555 | 1 - 426 | 1455 | Glu-1 to Gly-9, Asn-17 to Lys-22, Asp-30 to Phe-36, Lys-43 to Glu-49, Pro-133 to Lys-142. | AR061: 3, AR089: 2 | | |
| 546 | HSLFG13 | 847314 | 556 | 154 - 705 | 1456 | | AR089: 1, AR061: 0 S0028: 1 and S3018: 1. | | |
| 547 | HDAAS21 | 850577 | 557 | 2 - 724 | 1457 | Leu-26 to Cys-37, Cys-127 to Glu-132. | AR061: 158, AR089: 3 H0497: 2, L0766: 2, L0777: 2, H0589: 1, L0627: 1, L0779: 1, L0759: 1, L0604: 1 and H0506: 1. | | |
| 548 | HARMH10 | 852701 | 558 | 736 - 146 | 1458 | Gln-1 to Pro-6. | AR089: 9, AR061: 3 H0592: 1, S0150: 1, H0521: 1 and L0740: 1. | | |
| 549 | HSDAI07 | 859237 | 559 | 72 - 623 | 1459 | Ser-10 to Cys-16. | AR089: 1, AR061: 0 | | |

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| 550 | HLDQU41 | 864996 | 560 | 1 - 504 | 1460 | Glu-62 to Arg-69, Ser-140 to Thr-146. | S0126: 2, S0031: 2 and S0045: 1. AR061: 765, AR089: 3 L0803: 10, L0439: 5, L0617: 2, L0774: 2, L0438: 2, L0742: 2, L0747: 2, H0574: 1, H0510: 1, H0038: 1, L0804: 1, L0775: 1, L0789: 1 and L0581: 1. | | |
| 551 | HABU06 | 864997 | 561 | 20 - 937 | 1461 | Ser-29 to Ser-38, Ser-63 to Thr-69, Glu-90 to Asp-97; Phe-127 to Glu-135, His-215 to His-229, Asp-245 to Asp-257. | AR089: 4, AR061: 2 H0359: 1 and H0561: 1. | | |
| 552 | HSLDO63 | 866332 | 562 | 3 - 521 | 1462 | Trp-14 to Asn-30, Val-44 to Leu-50, Leu-116 to Tyr-121, Ser-164 to Thr-172. | AR061: 4, AR089: 4 S0028: 1 and H0542: 1. | | |
| 553 | HNHAG26 | 866694 | 563 | 251 - 880 | 1463 | | AR061: 7, AR089: 2 | | |
| 554 | HGBBC61 | 867065 | 564 | 449 - 3 | 1464 | | AR089: 1, AR061: 0 H0416: 1, H0181: 1, H0617: 1 and H0316: 1. | | |
| 555 | HMAEM27 | 870252 | 565 | 3 - 716 | 1465 | | AR089: 88, AR061: 44 H0494: 1, S0144: 1, L0749: 1, L0605: 1 and L0593: 1. | | |
| 556 | HEBCK42 | 875541 | 566 | 313 - 74 | 1466 | Glu-1 to Lys-6, | AR089: 26, AR061: 9 10q11.1-q24 | 157640, | |

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| | | | | | | Lys-15 to Asp-25. | | H0031: 4, S0007: 1 and L0748: 1. | | 174900, 180250, 186770, 188550, 236730, 271245, 278000, 278000, 600095, 600512, 600835, 601107, 601130, 602082 |
| 557 | HELNF03 | 881180 | 567 | 323 - 736 | 1467 | Arg-8 to Met-21, Ser-32 to Ala-37. | | AR089: 2, AR061: 1 H0381: 2, H0617: 2, S0045: 1 and S0044: 1. | | |
| 558 | HKINF95 | 882308 | 568 | 1 - 270 | 1468 | | | AR061: 399, AR089: 71 H0069: 1, H0399: 1, S0428: 1, H0698: 1 and H0521: 1. | | |
| 559 | HTLHE85 | 883263 | 569 | 1 - 663 | 1469 | Tyr-20 to Trp-25, Leu-39 to Ser-44, Asp-62 to Thr-79. | | AR089: 18, AR061: 13 H0618: 2, H0013: 1 and H0424: 1. | | |
| 560 | HTEOE72 | 886412 | 570 | 1 - 675 | 1470 | Thr-2 to Ser-9, Pro-23 to Arg-30, Pro-44 to Arg-49, Ser-62 to Pro-73, Phe-150 to Lys-155, | | AR050: 14, AR051: 12, AR054: 10, AR061: 6, AR089: 3 H0038: 2, H0616: 1, S0152: 1 and S0242: 1. | | |

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| 561 | HELENI3 | 907599 | 571 | 318 - 659 | 1471 | Asp-164 to Glu-169, Leu-191 to Val-198. Glu-13 to Trp-22, Gln-60 to Lys-65. | AR089: 1, AR061: 1 S0045: 1, S0144: 1, S0028: 1 and S0260: 1. | | |
| 562 | HFIE03 | 914882 | 572 | 1762 - 1052 | 1472 | Pro-11 to Asn-16, Lys-67 to His-75, Gly-145 to Trp-152, Glu-171 to Arg-176, Met-220 to Glu-230. | AR089: 15, AR061: 6 L0766: 3, L0596: 2, S0134: 1, H0327: 1, T0010: 1, H0616: 1, H0551: 1, L0363: 1, L0783: 1, H0520: 1, S0152: 1, H0555: 1, L0748: 1, L0439: 1, S0194: 1, H0423: 1 and H0506: 1. | | |
| 563 | HABGE01 | 915743 | 573 | 2 - 1276 | 1473 | Leu-39 to Lys-47, Gly-67 to Thr-76, Thr-86 to Thr-96. | AR089: 0, AR061: 0 | | |
| 564 | HWLKM02 | 917409 | 574 | 1012 - 11 | 1474 | Ala-2 to Glu-7, Leu-9 to Pro-17, Pro-30 to Glu-41, Gln-50 to Gly-56. | AR089: 3, AR061: 2 S0358: 5, H0617: 4, H0559: 3, L0804: 2, L0805: 2, H0657: 1, S0007: 1, H0455: 1, H0618: 1, H0546: 1, H0545: 1, H0488: 1, L0637: 1, L0775: 1, L0809: 1, L0789: 1, L0438: 1, L0439: 1, L0752: 1 and L0757: 1. | | |
| 565 | HOVERI3 | 917564 | 575 | 122 - 904 | 1475 | Gly-27 to Ala-33 | AR089: 5, AR061: 2 | | |

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| 566 | HE8UB94 | 920288 | 576 | 187 - 561 | 1476 | Gly-16 to Glu-21. | Leu-45 to Asn-53, Lys-86 to Ala-91, Ala-132 to Arg-137, Lys-174 to Phe-183, Gln-200 to Pro-207, Asp-251 to Gln-256. | L0779: 4, H0428: 3, L0773: 2, L0662: 2, L0659: 2, L0602: 2, L0777: 2, L0596: 2, L0608: 2, H0170: 1, H0580: 1, S0045: 1, T0048: 1, H0052: 1, L0471: 1, H0628: 1, L0770: 1, L0761: 1, L0805: 1, L0653: 1, L0657: 1, L0512: 1, H0682: 1, H0672: 1, L0748: 1, L0740: 1, L0749: 1, L0757: 1, S0031: 1, H0543: 1 and H0677: 1. | | |
| | | | | | | | | AR061: 2, AR089: 1 L0750: 7, L0777: 7, H0013: 6, L0805: 6, H0521: 4, L0596: 4, H0014: 3, L0756: 3, H0170: 2, S0360: 2, H0051: 2, H0622: 2, H0090: 2, S0002: 2, H0529: 2, L0776: 2, L0655: 2, L0606: 2, H0520: 2, H0547: 2, L0755: 2, L0759: 2, L0485: 2, L0604: 2, S0026: 2, H0171: 1. | | |

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| 567 | HTHDJ23 | 921274 | 577 | 1368 - 1739 | 1477 | Ser-25 to Lys-30. | S0116: 1, H0341: 1, S0045: 1, S0222: 1, S6014: 1, H0431: 1, H0587: 1, H0331: 1, H0486: 1, H0156: 1, L0021: 1, S0049: 1, H0309: 1, H0046: 1, H0086: 1, H0123: 1, S0388: 1, H0687: 1, H0111: 1, H0598: 1, H0616: 1, H0264: 1, H0561: 1, H0538: 1, S0426: 1, L0637: 1, L0646: 1, L0764: 1, L0521: 1, L0364: 1, L0803: 1, L0775: 1, L0527: 1, L0666: 1, H0144: 1, S0374: 1, H0519: 1, H0690: 1, H0435: 1, H0648: 1, S0330: 1, S0152: 1, L0748: 1, L0751: 1, L0745: 1, L0747: 1, L0731: 1, L0758: 1, H0423: 1, H0422: 1 and S0462: 1. | | |
| | | | | | | | AR051: 27, AR050: 26, AR054: 22, AR061: 4, AR089: 4 S0358: 1, H0266: 1. | | |

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| 568 | HWHPB72 | 922580 | 578 | 454 - 768 | 1478 | Thr-10 to Val-15, Asp-35 to Leu-41. | H0687: 1, H0063: 1 and L0749: 1. AR089: 4, AR061: 3 L0438: 3, S0007: 2, S0134: 1, H0587: 1, H0497: 1, H0123: 1, H0428: 1, H0039: 1, H0551: 1, H0623: 1, H0509: 1, H0435: 1, H0518: 1, L0748: 1 and L0759: 1. | | |
| 569 | HSQFX64 | 922581 | 579 | 1 - 324 | 1479 | Glu-21 to Ser-27, Glu-74 to Val-88. | AR089: 11, AR061: 6 | | |
| 570 | HDABB84 | 922582 | 580 | 3 - 1760 | 1480 | Leu-58 to Asp-68, Thr-91 to Val-96, Asp-116 to Leu-122, Glu-220 to Ser-226. | AR089: 9, AR061: 1 H0056: 2, H0059: 2, L0800: 2, L0663: 2, L0602: 2, L0747: 2, L0588: 2, L0591: 2, L0592: 2, L0599: 2, H0686: 1, S0360: 1, S0132: 1, H0497: 1, S0280: 1, H0042: 1, S0036: 1, H0634: 1, L0351: 1, H0560: 1, S0448: 1, H0509: 1, H0529: 1, L0764: 1, L0794: 1, L0774: 1, L0775: 1, L0375: 1, L0809: 1, L0666: 1, S0374: 1, L0438: 1, | | |

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| | | | | | | | | H0547: 1, H0435: 1, H0651: 1, S0380: 1, L0748: 1, L0749: 1, L0779: 1, L0752: 1, L0731: 1, L0759: 1, H0543: 1, H0423: 1 and H0506: 1. | | | |
| 571 | HLHFN83 | 924110 | 581 | 3 - 263 | 1481 | | | AR089: 14, AR061: 8 H0510: 2, L0595: 2, H0657: 1, H0580: 1, H0619: 1, H0357: 1, H0632: 1, H0013: 1, H0024: 1, H0578: 1, H0591: 1, H0509: 1, L0769: 1, L0804: 1, L0805: 1, L0776: 1, H0521: 1, H0555: 1, L0740: 1, L0749: 1 and H0423: 1. | | | |
| 572 | HPCRR26 | 926401 | 582 | 870 - 253 | 1482 | Asp-10 to Thr-15, Leu-19 to Arg-26, Gly-120 to Asn-125, Lys-131 to Ser-139, Gly-169 to Lys-174, Glu-199 to Met-205. | | AR089: 1, AR061: 0 | | | |
| 573 | HCMSD61 | 927475 | 583 | 66 - 959 | 1483 | Arg-17 to Asn-23, Arg-90 to Gly-95, Leu-114 to Glu-121, Pro-153 to Asp-158, Thr-288 to Lys-295. | | AR061: 6, AR089: 5 L0775: 5, H0486: 3, H0648: 3, L0748: 3, L0758: 3, H0657: 2, S0358: 2, H0370: 2, | | | |

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|-----|---------|--------|-----|---------|------|-----------------|--|--|--|---|--|--|--|--|--|
| | | | | | | | | | | H0331: 2, H0040: 2, H0616: 2, S0152: 2, L0754: 2, L0747: 2, L0759: 2, S0192: 2, H0170: 1, H0664: 1, S0356: 1, S0222: 1, H0575: 1, H0196: 1, H0014: 1, H0373: 1, H0039: 1, H0622: 1, T0023: 1, L0483: 1, H0644: 1, L0142: 1, H0674: 1, H0090: 1, H0059: 1, S0422: 1, L0772: 1, L0768: 1, L0766: 1, L0774: 1, L0655: 1, H0547: 1, H0435: 1, H0659: 1, H0521: 1, S0027: 1, L0740: 1, L0756: 1, H0445: 1, L0593: 1, H0668: 1, L0462: 1 and H0352: 1. | | | | | |
| 574 | HCEEC58 | 933866 | 584 | 1 - 327 | 1484 | | | | | AR089: 110, AR061: 37 S0007: 3, S0354: 2, H0529: 2, H0645: 1, H0052: 1 and H0039: 1. | | | | | |
| 575 | HSYAD06 | 935334 | 585 | 1 - 765 | 1485 | | | | | AR061: 4, AR089: 3 | | | | | |
| 576 | HTSID53 | 943374 | 586 | 2 - 994 | 1486 | Arg-1 to Glu-6. | | | | AR089: 1, AR061: 1 | | | | | |

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| 577 | HRGDE77 | 948737 | 587 | 2 - 1051 | 1487 | Lys-25 to Arg-32, Gly-53 to Asn-61, Asn-116 to Glu-121, Thr-194 to Thr-199, Asn-209 to Thr-217. Arg-20 to Leu-28, Phe-57 to Arg-79. | H0522: 2, H0052: 1, H0412: 1, L0794: 1, L0803: 1, H0651: 1, H0521: 1, L0748: 1, L0749: 1 and L0752: 1. AR089: 12, AR061: 8 L0751: 10, L0748: 9, S0222: 6, L0438: 4, L0747: 4, S0356: 3, H0040: 3, S0344: 3, L0766: 3, L0809: 3, L0665: 3, S0380: 3, L0758: 3, H0624: 2, S0360: 2, S0010: 2, H0014: 2, H0399: 2, H0622: 2, S0038: 2, S0144: 2, S0002: 2, L0770: 2, L0803: 2, H0666: 2, L0439: 2, L0749: 2, L0596: 2, L0595: 2, S0218: 1, S0400: 1, H0483: 1, S0045: 1, H0619: 1, H0393: 1, S0278: 1, H0250: 1, H0618: 1, H0253: 1, H0052: 1, H0457: 1, H0123: 1, H0242: 1, H0266: 1, H0687: 1, H0264: 1, H0102: 1 H0641: 1 | | |
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| 578 | HEGAU68 | 950009 | 588 | 239 - 520 | 1488 | | | H0646: 1, L0763: 1, L0771: 1, L0794: 1, L0804: 1, L0776: 1, L0807: 1, L0788: 1, L0664: 1, S0052: 1, H0144: 1, H0547: 1, H0689: 1, H0659: 1, H0648: 1, H0521: 1, H0696: 1, H0134: 1, L0779: 1 and L0605: 1. | | |
| | | | | | | | | AR089: 11, AR061: 4 L0744: 9, L0731: 8, L0439: 7, H0144: 5, L0749: 5, L0748: 4, L0745: 4, L0758: 4, S0040: 3, H0013: 3, H0038: 3, L0769: 3, L0773: 3, L0755: 3, H0306: 2, S0356: 2, S0358: 2, H0550: 2, H0392: 2, S0280: 2, H0620: 2, T0003: 2, H0598: 2, S0036: 2, H0623: 2, S0344: 2, S0002: 2, L0662: 2, L0768: 2, L0561: 2, L0775: 2, L0776: 2, L0527: 2, L0783: 2, L0438: 2, S0126: 2, H0539: 2, S0152: 2, | | |

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| H0521: 2, S3014: 2, L0754: 2, L0747: 2, L0780: 2, L0752: 2, L0757: 2, L0591: 2, L0608: 2, L0362: 2, L0361: 2, L0601: 2, L0603: 2, H0170: 1, H0265: 1, H0556: 1, T0002: 1, S0114: 1, L0427: 1, S0116: 1, S0282: 1, H0402: 1, S0420: 1, S0354: 1, S0376: 1, S0360: 1, H0208: 1, S0045: 1, S0132: 1, S0278: 1, H0549: 1, S0222: 1, S6014: 1, H0441: 1, H0438: 1, H0497: 1, H0333: 1, H0069: 1, L0021: 1, H0618: 1, S0010: 1, H0421: 1, H0251: 1, H0085: 1, H0327: 1, H0178: 1, H0050: 1, H0024: 1, H0051: 1, H0375: 1, H0594: 1, H0188: 1, H0687: 1, S0022: 1, H0252: 1, H0615: 1, H0428: 1, H0622: 1, H0031: 1, H0644: 1, H0673: 1, H0674: 1, |
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| 579 | HNGKH38 | 951032 | 589 | 3 - 251 | 1489 | H0135: 1, H0163: 1, H0634: 1, H0087: 1, H0412: 1, H0056: 1, S0038: 1, H0100: 1, T0041: 1, H0429: 1, S0450: 1, S0142: 1, S0426: 1, H0529: 1, L0763: 1, L0770: 1, L0796: 1, L0761: 1, L0667: 1, L0646: 1, L0764: 1, L0771: 1, L0766: 1, L0375: 1, L0655: 1, L0657: 1, L0659: 1, L0517: 1, L0383: 1, L0382: 1, L0543: 1, L0666: 1, L0664: 1, S0374: 1, H0520: 1, H0519: 1, H0689: 1, H0682: 1, H0659: 1, H0658: 1, S0328: 1, S0027: 1, L0740: 1, L0746: 1, L0750: 1, L0759: 1, H0445: 1, L0480: 1, L0584: 1, S0242: 1, S0276: 1, H0543: 1, H0423: 1, H0422: 1, S0446: 1, L0600: 1 and H0352: 1. | AR061: 11, AR089: 5 | | |
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| | | | | | | | | | H0069: 1, H0399: 1, S0428: 1, H0698: 1 and H0521: 1. | | | |
| 580 | HNEHNN26 | 952398 | 590 | 404 - 135 | 1490 | | | | AR089: 1, AR061: 0 S0216: 1 and S0390: 1. | | | |
| 581 | HTEHP64 | 953791 | 591 | 304 - 2 | 1491 | Asp-49 to Phe-54, Thr-89 to Ala-94. | | | AR089: 625, AR061: 610 L0666: 6, S6028: 3, L0662: 3, L0663: 3, H0038: 2, L0768: 2, S0360: 1, S0045: 1, H0574: 1, S0010: 1, H0428: 1, H0169: 1, S0036: 1, H0616: 1, L0520: 1, L0796: 1, L0657: 1, L0792: 1, L0665: 1, S0053: 1, H0547: 1, H0684: 1, S0260: 1, H0445: 1, L0599: 1 and L0593: 1. | 20q13.1 | 256540, 600281, 600281 | |
| 582 | HMILO78 | 953793 | 592 | 265 - 576 | 1492 | Ser-5 to Ser-12. | | | AR089: 11, AR061: 4 L0666: 6, S6028: 3, L0662: 3, L0663: 3, H0038: 2, L0768: 2, S0360: 1, S0045: 1, H0574: 1, S0010: 1, H0428: 1, H0169: 1, S0036: 1, H0616: 1, L0520: 1, L0796: 1, L0657: 1, L0792: 1, | 20q13.1 | 256540, 600281, 600281 | |

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| 583 | HFPCN94 | 955009 | 593 | 3 - 860 | 1493 | Pro-3 to Gly-10. | L0665: 1, S0053: 1, H0547: 1, H0684: 1, S0260: 1, H0445: 1, L0599: 1 and L0593: 1. AR089: 5, AR061: 4 L0731: 6, H0539: 5, L0065: 4, L0775: 4, L0803: 3, L0776: 3, L0663: 3, L0755: 3, S0356: 2, H0632: 2, H0545: 2, H0551: 2, L0769: 2, L0764: 2, L0662: 2, L0794: 2, L0783: 2, L0666: 2, L0750: 2, L0759: 2, H0624: 1, H0170: 1, H0583: 1, L0005: 1, H0580: 1, H0550: 1, S0222: 1, H0370: 1, H0586: 1, H0098: 1, H0318: 1, H0510: 1, H0622: 1, H0032: 1, H0169: 1, H0212: 1, S0036: 1, H0634: 1, H0022: 1, H0494: 1, S0422: 1, L0520: 1, L0796: 1, L0761: 1, L0373: 1, L0372: 1, L0806: 1, L0659: 1, L0809: 1, H0660: 1. | |
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| | | | | | | | | S0328: 1, S0380: 1, S0152: 1, H0696: 1, L0439: 1, L0754: 1, L0756: 1, L0777: 1, L0758: 1, H0445: 1, L0605: 1 and L0599: 1. | | | |
| 584 | HSLHV08 | 958582 | 594 | 167 - 3 | 1494 | | | AR089: 1, AR061: 0 S0428: 1 and S0028: 1. | | | |
| 585 | HPDVW40 | 961039 | 595 | 3 - 629 | 1495 | | Thr-85 to Gly-92, Pro-159 to Asn-180. | AR089: 13, AR061: 7 L0804: 5, L0758: 5, L0740: 3, L0754: 3, L0777: 3, L0604: 3, L0770: 2, L0794: 2, H0658: 2, L0752: 2, L0759: 2, L0622: 1, T0060: 1, L0021: 1, T0001: 1, L0163: 1, H0553: 1, L0769: 1, L0662: 1, L0659: 1, L0529: 1, L0789: 1, L0792: 1, S0330: 1, L0747: 1, L0749: 1 and L0485: 1. | 19 | | |
| 586 | HEMFC70 | 961963 | 596 | 1 - 1164 | 1496 | | Leu-28 to Asp-35, Leu-59 to Ser-65, Glu-111 to Lys-117, Gln-131 to Ala-137, Asp-224 to Asp-233, Ala-262 to Trp-268. | AR089: 8, AR061: 5 S0046: 2, S0116: 1, S0356: 1, H0194: 1, H0051: 1, H0591: 1, H0634: 1, H0551: 1, L0564: 1, S0150: 1, H0538: 1, S0152: 1, | | | |

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| 587 | HLDOO20 | 910371 | 597 | 2 - 157 | 1497 | Pro-21 to Arg-28. | AR061: 5, AR089: 4 L0748: 2, L0749: 2, H0510: 1 and H0144: 1. | | |
| | | 963284 | 886 | 24 - 1298 | 1786 | Glu-29 to Gly-35, Leu-51 to Glu-59, Gly-91 to His-98. | | | |
| | | 963655 | 887 | 1 - 1281 | 1787 | | | | |
| 588 | HSLEP67 | 963505 | 598 | 44 - 352 | 1498 | | AR061: 0, AR089: 0 S0428: 1, S0390: 1 and S0028: 1. | | |
| 589 | HSLEP94 | 964463 | 599 | 429 - 1355 | 1499 | | AR061: 2, AR089: 1 S0028: 5, H0624: 2, S0031: 2, H0171: 1, S0282: 1, H0250: 1, H0617: 1, H0124: 1, H0059: 1, H0144: 1, S0146: 1 and S0260: 1. | | |
| 590 | HSENS89 | 964527 | 600 | 1 - 891 | 1500 | Leu-1 to Phe-16. | AR089: 5, AR061: 3 H0556: 2, S0218: 1, S0132: 1, H0553: 1, H0494: 1, S0126: 1, L0602: 1, S0027: 1, L0748: 1, H0667: 1, S0276: 1 and H0423: 1. | | |
| 591 | HNTAF77 | 966190 | 601 | 509 - 3 | 1501 | | AR089: 1, AR061: 1 L0771: 3, S0222: 2, L0731: 2, H0295: 1, H0606: 1, L0770: 1. | | |

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| 592 | HBIOV48 | 967566 | 602 | 25 - 537 | 1502 | Ser-6 to Trp-15, Lys-18 to Gln-27, Pro-29 to Gly-35. | L0783: 1, L0791: 1, H0519: 1, L0751: 1, L0779: 1, L0755: 1 and L0759: 1. AR089: 0, AR061: 0 L0771: 4, L0803: 4, L0742: 4, L0770: 3, L0759: 3, H0194: 2, L0805: 2, L0776: 2, L0809: 2, L0789: 2, S0126: 2, S0328: 2, L0748: 2, L0779: 2, H0556: 1, S0354: 1, H0261: 1, S0010: 1, S0049: 1, H0052: 1, L0738: 1, H0105: 1, S0036: 1, H0135: 1, H0551: 1, H0538: 1, L0769: 1, L0761: 1, L0766: 1, L0649: 1, L0804: 1, L0774: 1, L0775: 1, L0659: 1, L0782: 1, L0787: 1, L0665: 1, H0593: 1, H0660: 1, H0672: 1, S0380: 1, L0741: 1, L0749: 1 and H0423: 1. | | | | |
| 593 | HBGMN45 | 967744 | 603 | 2 - 562 | 1503 | | AR089: 1, AR061: 1 H0617: 2, S6028: 1 and S0028: 1 | | | | |

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| 594 | HBXCE20 | 970889 | 604 | 2 - 403 | 1504 | | AR089: 1, AR061: 0 S0031: 4, H0624: 2, S0050: 2, H0246: 1, S0038: 1 and S0260: 1. | | |
| 595 | HSLJU88 | 780811 | 605 | 214 - 540 | 1505 | Ser-29 to Gly-35, Thr-82 to Val-95. | AR061: 1, AR089: 1 S0390: 2, S0278: 1 and S0144: 1. | | |
| 596 | HKGDQ60 | 863330 | 606 | 768 - 223 | 1506 | Arg-1 to His-9, Pro-14 to Thr-20. | AR089: 5, AR061: 2 H0261: 3, H0046: 3, L0485: 2, H0052: 1, H0538: 1 and L0745: 1. | | |
| 597 | HSDKF67 | 933059 | 607 | 2 - 469 | 1507 | Asn-2 to Asp-7. | AR061: 4, AR089: 1 H0271: 1 and S0260: 1. | | |
| 598 | HSLFT94 | 603023 | 608 | 3 - 323 | 1508 | Lys-16 to Arg-23, Gln-55 to Ile-62, Pro-99 to Asn-105. | AR089: 1, AR061: 1 S0028: 2 and S0044: 1. | | |
| 599 | HTJMD06 | 837603 | 609 | 2 - 424 | 1509 | Lys-35 to Lys-41, Asp-82 to Arg-88, Thr-123 to Thr-128. | AR089: 2, AR061: 1 S6028: 1, H0488: 1 and H0056: 1. | | |
| 600 | HNTBH68 | 851274 | 610 | 1 - 540 | 1510 | Ala-51 to Ser-57, Glu-108 to Trp-113, Phe-138 to Glu-146. | AR089: 6, AR061: 3 L0005: 1, H0144: 1, L0438: 1, H0519: 1, H0539: 1 and L0439: 1. | | |
| 601 | HMEKO39 | 863507 | 611 | 2 - 610 | 1511 | Pro-67 to Pro-72. | AR061: 5, AR089: 3 L0741: 5, L0751: 4, L0777: 4, S0007: 3, H0575: 3, L0747: 3, L0592: 3, S0212: 2, H0545: 2, H0266: 2, L0769: 2, L0771: 2, | | |

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|-----|---------|--------|-----|----------|------|--|--|--|---|--|--|--|--|
| | | | | | | | | | L0768: 2, L0794: 2, L0789: 2, H0144: 2, L0352: 2, S0028: 2, L0742: 2, L0439: 2, L0754: 2, L0779: 2, L0755: 2, S0418: 1, S0420: 1, S0376: 1, S0300: 1, H0438: 1, H0327: 1, H0009: 1, H0123: 1, H0594: 1, H0179: 1, H0271: 1, H0615: 1, H0628: 1, H0551: 1, S0038: 1, H0100: 1, S0464: 1, S0210: 1, L0369: 1, L0761: 1, L0800: 1, L0764: 1, L0521: 1, L0806: 1, L0659: 1, L0809: 1, L0367: 1, H0435: 1, S0152: 1, H0696: 1, L0756: 1, L0757: 1 and L0758: 1. | | | | |
| 602 | HAABH11 | 965473 | 612 | 1 - 699 | 1512 | | | | AR089: 16, AR061: 5 L0740: 5, H0356: 2, H0413: 2, L0770: 2, L0777: 2, S0376: 1, S0360: 1, H0646: 1, L0763: 1 and L0747: 1. | | | | |
| 603 | HUVFZ43 | 910860 | 613 | 3 - 1376 | 1513 | Lys-68 to Lys-75, Lys-111 to Asn-120. | | | AR089: 13, AR061: 4 H0619: 2, H0056: 2, | | | | |

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|-----|---------|--------|-----|------------|------|---|--|------|-------------------|
| | | | | | | Ser-137 to Leu-153, Gln-155 to Gly-162, Glu-169 to Gln-178, Ser-208 to Thr-213, Arg-239 to Gly-247, Lys-253 to Leu-259, Glu-275 to Glu-281. | S0132: 1, H0266: 1, H0623: 1, H0494: 1, L0769: 1 and S0152: 1. | | |
| 604 | HCEPH84 | 910864 | 614 | 1689 - 706 | 1514 | Ser-65 to Gly-75, Thr-84 to Ser-89. | AR089: 1, AR061: 1 L0439: 6, L0745: 5, H0052: 4, L0438: 4, L0592: 3, L0604: 3, H0009: 2, S0001: 1, H0599: 1, H0196: 1, H0172: 1, T0010: 1, S0364: 1, S0366: 1, S0038: 1, L0789: 1, H0144: 1, S0044: 1, L0747: 1, L0759: 1 and L0605: 1. | | |
| 605 | HNFDO52 | 916260 | 615 | 2 - 358 | 1515 | | AR089: 5, AR061: 5 H0083: 17, H0556: 14, H0265: 7, L0794: 6, H0271: 5, H0543: 5, L0766: 4, L0809: 4, H0635: 2, H0150: 2, S0114: 1, H0650: 1, H0645: 1, S0222: 1, H0438: 1, H0196: 1, H0594: 1, H0416: 1, H0615: 1, H0033: 1, | 2q11 | 129490, 600334 |

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|-----|---------|--------|-----|-----------|------|--|---|--------------------|--|
| 606 | HHETR23 | 919082 | 616 | 864 - 205 | 1516 | Lys-47 to Ile-60, Ser-102 to Lys-107, Lys-152 to Ser-158, Lys-171 to Glu-176. | H0087: 1, H0488: 1, S0142: 1, L0764: 1, L0803: 1, L0655: 1, L0657: 1, L0656: 1, L0659: 1, L0783: 1, L0790: 1, L0663: 1, L0665: 1, S0216: 1, H0670: 1, H0436: 1, L0758: 1, H0595: 1, H0542: 1 and H0422: 1. | Xp11.22- p11.21 | 300008, 300008, 300008, 300008, 300047, 301000, 301000, 301300, 301830, 305400, 308300, 309470, 309500, 309610, 311050 |
| | | | | | | | AR089: 1, AR061: 0 L0758: 5, S0360: 3, L0768: 3, S0380: 3, L0731: 3, H0038: 2, S0372: 2, L0761: 2, L0766: 2, H0539: 2, L0755: 2, H0341: 1, S0110: 1, S0418: 1, H0637: 1, S0278: 1, S0222: 1, H0052: 1, L0040: 1, H0252: 1, H0169: 1, H0616: 1, H0560: 1, S0382: 1, L0763: 1, L0770: 1, L0769: 1, L0646: 1, L0764: 1, L0803: 1, L0804: 1, L0775: 1, L0518: 1, L0809: 1, L0529: 1, L0791: 1, L0664: 1, H0659: 1, | | |

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| | | | | | | | | | H0648: 1, S0406: 1, L0751: 1, L0754: 1, L0779: 1, L0757: 1, L0597: 1, H0667: 1, S0242: 1, H0542: 1, H0543: 1 and L0698: 1. | | | |
| 607 | HMTAX31 | 971343 | 617 | 1091 - 522 | 1517 | Lys-24 to Lys-36, Asp-63 to Thr-70, Arg-139 to Lys-146, Leu-156 to Ala-171. | | | AR050: 40, AR051: 39, AR054: 37, AR089: 5, AR061: 1 L0777: 4, S0358: 2, S0126: 2, H0522: 2, S0116: 1, H0638: 1, H0443: 1, H0014: 1, H0379: 1, S0016: 1, S0374: 1, H0518: 1, H0521: 1 and L0740: 1. | | | |
| 608 | HKIY174 | 729217 | 618 | 3 - 347 | 1518 | Tyr-14 to Ser-22. | | | AR061: 5, AR089: 3 S0045: 1, H0441: 1, H0590: 1 and L0741: 1. | | | |
| 609 | HSKEI21 | 760792 | 619 | 398 - 3 | 1519 | Tyr-12 to Gly-19, Ser-90 to Pro-98. | | | AR061: 171, AR089: 34 L0751: 12, H0556: 9, L0596: 9, L0372: 5, H0265: 4, L0803: 4, S0404: 4, L0748: 4, L0758: 4, H0135: 3, L0665: 3, H0521: 3, L0742: 3, H0656: 2, H0341: 2, H0255: 2, S0418: 2, S0376: 2, | | | |

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| | | | | | | L0645: 1, L0662: 1, L0626: 1, L0768: 1, L0794: 1, L0766: 1, L0388: 1, L0774: 1, L0806: 1, L0776: 1, L0659: 1, H0547: 1, H0519: 1, H0435: 1, H0672: 1, H0651: 1, S0330: 1, H0539: 1, H0518: 1, S0350: 1, H0134: 1, S012: 1, S0037: 1, S014: 1, S0028: 1, L0743: 1, L0744: 1, L0747: 1, L0750: 1, L0777: 1, L0780: 1, L0731: 1, L0587: 1, H0668: 1, S0196: 1, H0542: 1, H0422: 1, S0460: 1 and H0506: 1. | | | | |
| 610 | HKA FK68 | 869127 | 620 | 605 - 18 | 1520 | AR089: 3, AR061: 3 L0751: 12, H0556: 9, L0596: 8, L0372: 5, H0265: 4, L0803: 4, S0404: 4, L0748: 4, L0758: 4, H0135: 3, L0665: 3, H0521: 3, L0742: 3, H0656: 2, H0341: 2, H0255: 2, S0418: 2, S0376: 2. | | | | |

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| 611 | HSRBB92 | 905110 | 621 | 2 - 2011 | 1521 | <p>Leu-11 to Asn-16, Gly-164 to Glu-171, Leu-181 to Ser-186, Asp-193 to Ser-201, Glu-222 to Leu-229, Gln-238 to Tyr-245, Leu-256 to Asp-267, Gly-286 to Gln-301, Ser-311 to Ala-319, Glu-345 to Gly-351,</p> | <p>L0645: 1, L0662: 1, L0626: 1, L0768: 1, L0794: 1, L0766: 1, L0388: 1, L0774: 1, L0806: 1, L0776: 1, L0659: 1, H0547: 1, H0519: 1, H0435: 1, H0672: 1, H0651: 1, S0330: 1, H0539: 1, H0518: 1, S0350: 1, H0134: 1, S3012: 1, S0037: 1, S3014: 1, S0028: 1, L0743: 1, L0744: 1, L0747: 1, L0750: 1, L0777: 1, L0780: 1, L0731: 1, L0587: 1, H0668: 1, S0196: 1, H0542: 1, H0422: 1, S0460: 1 and H0506: 1.</p> | <p>AR089: 23, AR061: 4 L0779: 10, L0747: 8, L0758: 7, L0766: 4, L0776: 4, L0748: 4, L0740: 4, S0360: 3, H0616: 3, L0754: 3, L0731: 3, L0759: 3, L0599: 3, L0362: 3, H0543: 3, H0341: 2, H0013: 2, H0024: 2,</p> | <p>120260, 138140, 178300, 246450</p> |
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| 613 | HWLWQ87 | 932577 | 623 | 76 - 519 | 1523 | Glu-44 to Gly-50, Pro-104 to Gly-111, Gly-127 to Leu-132, Asn-146 to Asp-151, Asn-165 to Glu-170, Ser-194 to Asp-202. Ile-11 to Glu-19. | S0358: 1, H0370: 1, H0253: 1, H0040: 1, H0547: 1, L0601: 1 and S0196: 1. AR089: 23, AR061: 12 L0731: 6, L0766: 5, L0759: 5, L0471: 2, H0038: 2, L0748: 2, L0740: 2, L0758: 2, L0590: 2, S0360: 1, H0596: 1, H0046: 1, L0483: 1, H0644: 1, H0616: 1, H0509: 1, H0647: 1, S0210: 1, L0648: 1, L0363: 1, L0774: 1, L0775: 1, L0657: 1, L0526: 1, L0666: 1, L0664: 1, S0126: 1, H0672: 1, L0744: 1, L0593: 1, L0595: 1, H0665: 1 and S0194: 1. | | |
| 614 | H6EEP53 | 942872 | 624 | 3 - 1595 | 1524 | | AR061: 1, AR089: 1 L0748: 8, L0769: 7, L0758: 7, L0749: 5, H0135: 4, S0418: 3, S0358: 3, H0618: 3, H0424: 3 H0529: 3 | | |

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| 616 | HFHXHD52 | 490721 | 626 | 191 - 3 | 1526 | Asn-44 to Ala-51. | H0624: 2 and S0031: 1. S0001: 1, S0045: 1 and S0216: 1. | | |
| | | 883683 | 888 | 1 - 279 | 1788 | Phe-2 to Ser-8, Glu-58 to Gln-63, Asn-74 to Leu-81. | | | |
| 617 | HPMAM67 | 915879 | 627 | 2 - 64 | 1527 | | L0777: 20, L0439: 11, L0747: 10, S0360: 6, L0766: 6, L0758: 6, L0717: 5, H0521: 5, H0038: 3, S0330: 3, L0752: 3, L0755: 3, L0599: 3, S0358: 2, H0581: 2, S0003: 2, S0214: 2, H0068: 2, L0764: 2, L0662: 2, L0655: 2, L0666: 2, L0665: 2, H0648: 2, L0740: 2, L0751: 2, L0749: 2, L0750: 2, L0731: 2, L0757: 2, S0031: 2, L0596: 2, L0581: 2, L0362: 2, S0192: 2, H0542: 2, S0040: 1, H0650: 1, H0657: 1, S0282: 1, H0580: 1, H0393: 1, H0586: 1, H0574: 1, H0486: 1, L0586: 1, H0013: 1, L0021: 1, | | |

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| | | | | | | | | Lys-57 to Pro-62, Ser-108 to Ala-114, Asp-133 to Arg-140, Arg-173 to Asn-183. | L0608: 3, H0624: 1, H0589: 1, H0438: 1, H0250: 1, S0050: 1, H0135: 1, S0144: 1, H0689: 1 and S0028: 1. | | |
| | | | | | | | | Cys-32 to Cys-39, Glu-47 to Pro-52, Lys-57 to Pro-62, Ser-108 to Ala-114, Asp-133 to Arg-140, Arg-173 to Asn-183. | | | |
| | | | | | | | | Asp-72 to Glu-78, Ser-103 to Glu-110, Lys-112 to His-117. | | | |
| | | | | | | | | Lys-42 to Pro-47, Ser-93 to Ala-99, Asp-118 to Arg-125, Arg-158 to Asn-168, Ala-251 to Val-263, His-287 to Tyr-292, Glu-302 to Gln-307. | | | |
| 619 | HELGMI94 | 913938 | 629 | 1 - 1437 | 1529 | | | Gly-1 to Ser-8, Arg-10 to Ser-15, Leu-17 to Gly-22, Lys-115 to Ala-130, Tyr-149 to Gly-156, Asn-181 to Glu-190, Glu-252 to Glu-257, Ser-339 to Asp-347, Leu-356 to Leu-361, | AR089: 9, AR061: 5 H0584: 5, H0599: 5, H0556: 4, H0124: 4, H0559: 3, H0622: 3, H0341: 2, H0125: 2, S0045: 2, H0620: 2, H0024: 2, T0042: 2, L0665: 2, H0144: 2, H0265: 1, S6024: 1, | 16p11.2 | 147781, 172471, 182381 |
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| | | | | | | Ser-387 to Lys-395, Thr-470 to Ile-476. | H0583: 1, H0208: 1, S0046: 1, H0393: 1, S0278: 1, H0549: 1, H0550: 1, H0438: 1, H0586: 1, H0486: 1, H0250: 1, S0280: 1, H0618: 1, H0253: 1, H0009: 1, H0687: 1, H0284: 1, H0424: 1, H0031: 1, S0366: 1, H0116: 1, H0056: 1, S0038: 1, H0494: 1, H0132: 1, H0131: 1, H0130: 1, L0662: 1, L0803: 1, S0428: 1, S0216: 1, S0126: 1, H0518: 1, S0152: 1, S0118: 1, S014: 1, L0759: 1 and S0011: 1. | | | |
| 620 | HLJDQ52 | 923110 | 630 | 3 - 824 | 1530 | Gly-26 to Val-70, Ser-199 to Arg-204. | AR089: 15, AR061: 1 T0109: 1, H0013: 1, H0375: 1, H0509: 1, H0519: 1, H0690: 1, S0152: 1 and L0485: 1. | | | |
| 621 | HAAW40 | 1219455 | 631 | 68 - 2323 | 1531 | Pro-7 to Arg-12, Leu-32 to His-52, Tyr-54 to Asp-69, Pro-74 to Gly-92, Glu-99 to Arg-125, Asp-130 to Glu-142. | AR089: 4, AR061: 1 L0803: 5, L0731: 4, L0662: 3, L0665: 3, S0276: 3, H0486: 2, H0575: 2, H0318: 2, L0794: 2, L0805: 2, | | | |

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| 622 | HATAZ67 | 1106635 | 893 | 1 - 765 | 1793 | <p>Thr-144 to Ala-153, Arg-197 to Lys-202, Leu-214 to Pro-227, Asp-245 to Arg-251, Gly-261 to Gln-267, Gly-283 to His-288, Ser-326 to Gln-336, Met-356 to Glu-361, Ala-438 to Ile-444, Ser-479 to Val-484, Arg-490 to Arg-499, Pro-509 to Gln-514, Glu-622 to Ser-628, Thr-653 to Arg-658, Glu-678 to Asp-752.</p> | <p>L0776: 2, L0809: 2, L0663: 2, H0684: 2, L0740: 2, L0759: 2, L0592: 2, H0624: 1, L0448: 1, H0341: 1, S0282: 1, H0663: 1, S0360: 1, H0580: 1, L0468: 1, H0587: 1, H0427: 1, S0010: 1, L0471: 1, H0644: 1, H0169: 1, L0456: 1, H0090: 1, H0264: 1, H0412: 1, H0561: 1, S0150: 1, S0002: 1, H0529: 1, L0638: 1, L0372: 1, L0649: 1, L0388: 1, L0659: 1, L0783: 1, L0789: 1, L0791: 1, H0519: 1, S0380: 1, H0522: 1, H0436: 1, L0747: 1, L0752: 1, L0757: 1, L0599: 1, H0542: 1, H0543: 1 and H0422: 1.</p> | | |
| | | 825697 | 893 | 1 - 765 | 1793 | | | | |
| | | 1106635 | 632 | 2 - 598 | 1532 | <p>Asn-25 to Trp-34, Ile-51 to Asp-58, Gln-87 to Pro-93.</p> | <p>AR061: 0, AR089: 0 H0038: 3, H0156: 2, L0455: 1, H0616: 1, S0038: 1, H0538: 1 and S0028: 1</p> | | |

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| 623 | HBUCAC02 | 908326 | 894 | 3 - 809 | 1794 | Asn-23 to Trp-32, Ile-49 to Asp-56, Gln-85 to Pro-91. | AR089: 13, AR061: 8 S0152: 4, H0556: 3, H0265: 2, S3014: 2, H0543: 2, H0423: 2, H0161: 1, H0650: 1, H0402: 1, S0045: 1, S0046: 1, H0393: 1, H0599: 1, H0575: 1, H0618: 1, H0253: 1, S0182: 1, H0083: 1, H0594: 1, H0247: 1, H0124: 1, H0652: 1, S0144: 1, H0519: 1, H0651: 1, S0027: 1 and H0445: 1. | | | |
| | | 1220017 | 633 | 3 - 668 | 1533 | Ala-8 to Thr-23, Pro-35 to Met-41, Asn-60 to Thr-65, Asn-89 to Glu-94, Pro-161 to Leu-167, Asp-184 to Trp-189, Phe-192 to Leu-206, Arg-215 to Leu-221. | | | | |
| | | 933546 | 895 | 3 - 818 | 1795 | Ala-8 to Thr-23, Pro-35 to Met-41, Asn-60 to Thr-65, Asn-89 to Glu-94, Pro-161 to Leu-167, Asp-184 to Trp-189, Phe-192 to Pro-201, Pro-226 to Lys-231, Ala-237 to Pro-264. | | | | |
| 624 | HCWEQ14 | 1117318 | 634 | 319 - 77 | 1534 | | AR089: 39, AR061: 8 H0305: 3 | | | |
| | | 908245 | 896 | 1 - 177 | 1796 | Leu-43 to Tyr-48. | | | | |

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|-----|---------|---------|-----|----------|------|---|--|--|
| 625 | HDPWH41 | 1228148 | 635 | 1 - 642 | 1535 | AR089: 6, AR061: 2 S0252: 5, S0268: 5, S0256: 4, S0228: 3, S0270: 3, S0258: 2, H0305: 2, H0090: 2, H0521: 2, L0740: 2, L0777: 2, H0657: 1, S0212: 1, H0661: 1, H0580: 1, L0717: 1, H0438: 1, H0486: 1, T0074: 1, H0581: 1, S0388: 1, H0412: 1, L0637: 1, L0766: 1, L0791: 1, S0216: 1, H0670: 1, S0380: 1, L0755: 1, H0445: 1, L0605: 1, L0592: 1, L0581: 1, L0593: 1 and H0543: 1. | | |
| 626 | HDQEH61 | 1213567 | 636 | 46 - 867 | 1536 | AR089: 63, AR061: 13 H0616: 3, H0521: 3, H0046: 2, H0038: 2, S0045: 1, H0550: 1, H0013: 1, S0386: 1, H0494: 1, S0150: 1, H0520: 1, H0436: 1 and L0595: 1. | | |
| | | 772569 | 897 | 1 - 369 | 1797 | Arg-68 to Ser-76. | | |
| | | 908303 | 898 | 2 - 766 | 1798 | Gln-49 to Thr-58, Pro-175 to Lys-184. | | |

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|-----|---------|---------|-----|-----------|------|---|---|---------|---|
| 627 | HDTDD72 | 587710 | 637 | 162 - 371 | 1537 | | AR089: 159, AR061: 142 H0486: 1 | 17p13.3 | 113721, 247200, 600059, 601545 |
| 628 | HFRBN02 | 1152485 | 638 | 2 - 967 | 1538 | Gly-114 to Gly-120, Pro-140 to Tyr-145, Asn-180 to Gly-185, Arg-274 to Ala-280, Gly-310 to Gly-317. | AR089: 3, AR061: 1 S0045: 1, S0050: 1, H0020: 1 and S0032: 1. | | |
| 629 | HKAHH72 | 973667 | 899 | 2 - 409 | 1799 | Gly-114 to Gly-120. | | | |
| | | 1107045 | 639 | 1 - 642 | 1539 | Pro-9 to Ala-19, Ser-39 to Gly-46, Thr-54 to Gly-62, Ile-77 to Arg-84, Thr-122 to Met-132, Gln-134 to Gln-147. | AR089: 2, AR061: 2 L0766: 2, L0665: 2, H0395: 1, S0212: 1, S0360: 1, H0551: 1, H0494: 1, L0639: 1, L0521: 1, L0804: 1, H0682: 1 and L0749: 1. | | |
| | | 761293 | 900 | 1 - 690 | 1800 | Pro-9 to Ala-19, Ser-39 to Gly-46, Thr-54 to Gly-62, Ile-77 to Arg-84, Thr-122 to Met-132, Gln-134 to Gln-147. | | | |
| 630 | HMAAD90 | 1152487 | 640 | 334 - 2 | 1540 | Ser-15 to Gln-23, Gly-79 to Asp-92, Gly-105 to Cys-111. | AR089: 2, AR061: 1 L0769: 7, L0783: 6, L0775: 5, L0748: 4, L0758: 4, L0622: 3, H0599: 3, H0373: 3, L0772: 3, L0777: 3, L0757: 3, S0045: 2, | | |

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| 631 | HMABQ71 | 1105540 | 641 | 3 - 374 | 1541 | His-173 to Asp-178, Arg-196 to Ser-202, Arg-214 to Val-220, Ser-243 to Leu-253, Arg-275 to Ile-283, Lys-367 to Phe-374, Gln-384 to Gly-389, Glu-430 to Lys-440. | AR089: 1, AR061: 0 S0144: 1 and H0521: 1. | | |
| 632 | HPJEV95 | 729831 1105131 | 902 642 | 189 - 497 82 - 405 | 1802 1542 | | AR061: 4, AR089: 1 S0152: 1 and L0601: 1. | | |
| 633 | HSKYR59 | 929723 1219545 | 903 643 | 82 - 408 154 - 783 | 1803 1543 | His-91 to Gly-103, Gly-112 to Gly-117, Glu-129 to Glu-136, Gly-146 to Gly-151, Arg-168 to Glu-184, Arg-203 to Arg-210. | AR061: 16, AR089: 6 H0617: 10, S0358: 5, L0622: 4, H0620: 4, H0658: 4, L0623: 3, H0424: 3, H0549: 2, H0550: 2, H0586: 2, H0486: 2, H0546: 2, L0769: 2, L0773: 2, S0374: 2, S0206: 2, L0743: 2, L0750: 2, L0779: 2, L0731: 2, L0601: 2, H0624: 1, H0170: 1, H0171: 1, H0686: 1, H0295: 1, H0657: 1, H0484: 1, H0255: 1, S0420: 1, | | |

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H0617: 10, S0358: 5,
L0622: 4, H0620: 4,
H0658: 4, L0623: 3,
H0424: 3, H0549: 2,
H0550: 2, H0586: 2,
H0486: 2, H0546: 2,
L0769: 2, L0773: 2,
S0374: 2, S0206: 2,
L0743: 2, L0750: 2,
L0779: 2, L0731: 2,
L0601: 2, H0624: 1,
H0170: 1, H0171: 1,
H0686: 1, H0295: 1,
H0657: 1, H0484: 1,
H0255: 1, S0420: 1,
S0376: 1, S0360: 1,
H0370: 1, H0455: 1,
H0587: 1, T0060: 1,
T0114: 1, H0599: 1,
H0122: 1, H0327: 1,
H0544: 1, H0545: 1,
H0188: 1, H0688: 1,
T0006: 1, H0213: 1,
H0606: 1, H0673: 1,
S0364: 1, S0366: 1,
H0634: 1, H0087: 1,
H0413: 1, H0334: 1,
S0144: 1, L0598: 1,
L0763: 1, L0796: 1,
L0639: 1, L0761: 1,
L0772: 1, L0373: 1.

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|-----|---------|---------|-----|------------|------|---|--|--|--|
| 635 | HSXCW82 | 933749 | 905 | 11 - 604 | 1805 | Ala-2 to Gly-15, Glu-120 to Ser-125. | L0764: 1, L0774: 1, L0775: 1, L0783: 1, L0809: 1, L0666: 1, L0663: 1, H0651: 1, S0378: 1, H0521: 1, S0392: 1, H0478: 1, L0751: 1, L0747: 1, L0752: 1, L0755: 1, L0757: 1, H0445: 1, L0608: 1, L0361: 1, L0366: 1, H0542: 1 and H0543: 1. | | |
| | | 1164013 | 645 | 123 - 1442 | 1545 | Leu-14 to Ile-19, Pro-69 to Pro-76, Glu-86 to Thr-91, Val-121 to Thr-127, Phe-183 to Gln-188, Gly-282 to Lys-291, Arg-337 to Asn-346. | AR061: 6, AR089: 5, H0556: 8, H0617: 6, L0659: 6, L0666: 6, L0596: 6, H0441: 5, L0665: 5, S0222: 4, T0010: 4, S0038: 4, H0657: 3, H0559: 3, H0013: 3, H0494: 3, L0804: 3, L0809: 3, H0547: 3, S0152: 3, H0521: 3, H0265: 2, H0656: 2, L0717: 2, S0278: 2, H0250: 2, H0575: 2, S0049: 2, H0620: 2, H0288: 2, H0213: 2, S0036: 2. | | |

H0634: 2, H0623: 2,
L0764: 2, L0766: 2,
L0775: 2, L0438: 2,
H0682: 2, S0028: 2,
L0779: 2, L0758: 2,
L0595: 2, H0422: 2,
H0224: 1, S0430: 1,
L0785: 1, H0341: 1,
S0212: 1, H0663: 1,
S0420: 1, H0637: 1,
H0580: 1, H0437: 1,
H0282: 1, H0249: 1,
T0109: 1, H0244: 1,
H0069: 1, S0346: 1,
H0318: 1, H0052: 1,
H0194: 1, N0006: 1,
L0471: 1, H0024: 1,
H0057: 1, L0163: 1,
H0107: 1, H0083: 1,
H0594: 1, S0336: 1,
H0070: 1, T0006: 1,
H0644: 1, H0181: 1,
H0135: 1, H0090: 1,
H0040: 1, H0087: 1,
H0059: 1, H0100: 1,
L0351: 1, T0041: 1,
H0429: 1, H0647: 1,
S0210: 1, S0002: 1,
H0529: 1, L0369: 1,
L0769: 1, L0761: 1,
0372: 1, L0800: 1.

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|-----|---------|--------|-----|-----------|------|---|--|---------------|---|
| 636 | HSYDB42 | 739372 | 906 | 115 - 387 | 1806 | Leu-14 to Ile-19. | L0794: 1, L0803: 1, L0806: 1, L0509: 1, L0657: 1, L0383: 1, L0787: 1, L0663: 1, S0374: 1, H0593: 1, H0658: 1, H0522: 1, H0134: 1, H0555: 1, L0612: 1, S3012: 1, S0037: 1, S3014: 1, S0206: 1, L0439: 1, L0749: 1, L0752: 1, S0031: 1, L0592: 1, L0608: 1, L0366: 1, H0667: 1, S0276: 1, H0542: 1 and H0423: 1. | 22q13.1-q13.2 | 103050, 103050, 124030, 124030, 138981, 182380, 188826, 190040, 190040, 190040 |
| | | 933545 | 646 | 2 - 631 | 1546 | Arg-1 to Thr-11, Pro-23 to Met-29, Asn-48 to Thr-53, Asn-77 to Glu-82, Pro-149 to Leu-155, Asp-172 to Trp-177, Phe-180 to Leu-194, Arg-203 to Leu-209. | AR061: 2, AR089: 1 H0305: 5, L0766: 3, L0748: 3, H0265: 2, H0556: 2, H0551: 2, H0494: 2, L0770: 2, L0758: 2, L0599: 2, L0361: 2, H0650: 1, H0657: 1, H0381: 1, H0419: 1, H0427: 1, H0618: 1, H0421: 1, H0530: 1, H0546: 1, H0413: 1, H0625: 1, L0369: 1, L0644: 1, L0521: 1, L0375: 1, | | |

| | | | | | | | | | |
|-----|---------|---------|-----|---------|------|--|--|--|--|
| 637 | HTXKJ79 | 1193059 | 647 | 2 - 421 | 1547 | Pro-3 to Leu-9, Glu-12 to Val-22, Gln-27 to Glu-33, Pro-68 to Glu-75. | L0783: 1, L0809: 1, L0789: 1, H0144: 1, S0374: 1, L0565: 1, H0658: 1, S0330: 1, H0539: 1, L0777: 1, L0731: 1, H0542: 1 and H0506: 1. AR089: 3, AR061: 3 L0748: 9, S0356: 8, S0358: 8, L0471: 5, H0144: 5, L0740: 5, H0543: 5, H0574: 4, H0556: 3, S0354: 3, S0360: 3, S0049: 3, H0083: 3, T0042: 3, H0494: 3, S0374: 3, H0134: 3, H0436: 3, H0624: 2, H0663: 2, S0007: 2, S0132: 2, H0486: 2, H0013: 2, H0036: 2, H0251: 2, H0009: 2, S0036: 2, H0412: 2, H0561: 2, S0142: 2, H0522: 2, L0750: 2, L0588: 2, H0159: 1, H0583: 1, H0656: 1, H0341: 1, S0212: 1, H0240: 1, H0125: 1, S0418: 1, S0420: 1, S0410: 1. | | |
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| | | | | | | | S0045: 1, H0411: 1, H0369: 1, H0586: 1, H0497: 1, H0643: 1, H0331: 1, S0010: 1, H0052: 1, H0327: 1, H0544: 1, H0545: 1, H0011: 1, H0012: 1, H0014: 1, H0015: 1, H0239: 1, H0266: 1, H0688: 1, H0124: 1, H0135: 1, H0040: 1, H0413: 1, H0059: 1, H0280: 1, S0344: 1, H0529: 1, H0691: 1, H0547: 1, H0519: 1, H0682: 1, H0660: 1, S0328: 1, H0518: 1, H0521: 1, S0037: 1, S3014: 1, S0028: 1, L0742: 1, L0752: 1, L0755: 1, S0026: 1, H0136: 1 and H0293: 1. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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|-----|---------|---------|-----|---------|------|---|--|--|--|--|
| | | | | | | | | | S0212: 1, H0661: 1, H0580: 1, L0717: 1, H0438: 1, H0486: 1, T0074: 1, H0581: 1, S0388: 1, H0412: 1, L0637: 1, L0766: 1, L0791: 1, S0216: 1, H0670: 1, S0380: 1, L0755: 1, H0445: 1, L0605: 1, L0592: 1, L0581: 1, L0593: 1 and H0543: 1. | |
| 639 | HUSZS75 | 1193982 | 908 | 2 - 517 | 1808 | Arg-1 to Asp-13, Arg-81 to Ser-89, Gly-128 to Gly-143. Arg-54 to Pro-67, Arg-82 to Ala-90, Gln-105 to Asp-115. | | | AR089: 1, AR061: 1 L0769: 10, L0754: 10, L0766: 5, L0803: 4, L0756: 4, L0779: 4, L0780: 4, L0748: 3, L0753: 3, H0620: 2, H0264: 2, L0770: 2, L0806: 2, L0741: 2, L0747: 2, L0604: 2, H0265: 1, H0556: 1, H0657: 1, H0656: 1, H0341: 1, H0392: 1, H0331: 1, H0559: 1, H0427: 1, L0021: 1, H0173: 1, H0052: 1, | |

| | | | | | | | | |
|-----|---------|-------------------|------------|----------------------|--------------|---|---|--|
| 640 | HWBDR25 | 908443 1174365 | 909 650 | 64 - 918 3 - 1259 | 1809 1550 | Arg-7 to Thr-13. Pro-1 to Glu-13, Gln-29 to Asn-35, Tyr-38 to Asn-43, Ala-102 to Ser-108, Arg-124 to Ile-134, Asp-172 to Asp-180, Lys-247 to Asn-252, Gly-336 to Trp-342. Lys-37 to Asn-42, Gly-126 to Trp-132. | AR089: 5, AR061: 1 H0551: 2, S0420: 1, H0580: 1, H0586: 1, S0002: 1, H0435: 1 and H0521: 1. | |
| 641 | HBGSS51 | 954855 | 651 | 341 - 3 | 1551 | | AR061: 5, AR089: 4 L0771: 12, H0040: 2, H0539: 2, H0306: 1, H0617: 1 and H0135: 1. | |

[42] The first column in Table 1A provides the gene number in the application corresponding to the clone identifier. The second column in Table 1A provides a unique "Clone ID NO:Z" for a cDNA clone related to each contig sequence disclosed in Table 1A. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.

[43] The third column in Table 1A provides a unique "Contig ID" identification for each contig sequence. The fourth column provides the "SEQ ID NO:" identifier for each of the contig polynucleotide sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred open reading frame (ORF) shown in the sequence listing and referenced in Table 1A, column 6, as SEQ ID NO:Y. Where the nucleotide position number "To" is lower than the nucleotide position number "From", the preferred ORF is the reverse complement of the referenced polynucleotide sequence.

[44] The sixth column in Table 1A provides the corresponding SEQ ID NO:Y for the polypeptide sequence encoded by the preferred ORF delineated in column 5. In one embodiment, the invention provides an amino acid sequence comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by "ORF (From-To)". Also provided are polynucleotides encoding such amino acid sequences and the complementary strand thereto.

[45] Column 7 in Table 1A lists residues comprising epitopes contained in the polypeptides encoded by the preferred ORF (SEQ ID NO:Y), as predicted using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). In specific embodiments, polypeptides of the invention comprise, or alternatively consist of, at least one, two, three, four, five or more of the predicted epitopes as described in Table 1A.

It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly.

[46] Column 8 in Table 1A provides an expression profile and library code: count for each of the contig sequences (SEQ ID NO:X) disclosed in Table 1A, which can routinely be combined with the information provided in Table 4 and used to determine the tissues, cells, and/or cell line libraries which predominantly express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the code and description provided in Table 4. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon) represents the number of times a sequence corresponding to the reference polynucleotide sequence was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression.

[47] Column 9 in Table 1A provides a chromosomal map location for certain polynucleotides of the invention. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Each sequence in the UniGene database is

assigned to a "cluster"; all of the ESTs, cDNAs, and STSs in a cluster are believed to be derived from a single gene. Chromosomal mapping data is often available for one or more sequence(s) in a UniGene cluster; this data (if consistent) is then applied to the cluster as a whole. Thus, it is possible to infer the chromosomal location of a new polynucleotide sequence by determining its identity with a mapped UniGene cluster.

[48] A modified version of the computer program BLASTN (Altshul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993)) was used to search the UniGene database for EST or cDNA sequences that contain exact or near-exact matches to a polynucleotide sequence of the invention (the 'Query'). A sequence from the UniGene database (the 'Subject') was said to be an exact match if it contained a segment of 50 nucleotides in length such that 48 of those nucleotides were in the same order as found in the Query sequence. If all of the matches that met this criteria were in the same UniGene cluster, and mapping data was available for this cluster, it is indicated in Table 1A under the heading "Cytologic Band". Where a cluster had been further localized to a distinct cytologic band, that band is disclosed; where no banding information was available, but the gene had been localized to a single chromosome, the chromosome is disclosed.

[49] Once a presumptive chromosomal location was determined for a polynucleotide of the invention, an associated disease locus was identified by comparison with a database of diseases which have been experimentally associated with genetic loci. The database used was the Morbid Map, derived from OMIM™ (*supra*). If the putative chromosomal location of a polynucleotide of the invention (Query sequence) was associated with a disease in the Morbid Map database, an OMIM reference identification number was noted in column 10, Table 1A, labelled "OMIM Disease Reference(s)". Table 5 is a key to the OMIM reference identification numbers (column 1), and provides a description of the associated disease in Column 2.

TABLE 1B

| Clone ID NO:Z | SEQ ID NO:X | CONTIG ID: | BAC ID: A | SEQ ID NO:B | EXON From-To |
|------------------|----------------|---------------|-----------|----------------|--|
| HADTU18 | 26 | 666268 | AC067849 | 1811 | 1-1270 |
| HADTU18 | 26 | 666268 | AC067849 | 1812 | 1-408 |
| HYAAH23 | 42 | 1032585 | AL158156 | 1813 | 1-134 381-1154 1539-2051 2660-4011 4082-4116 4578-5063 5736-6373 6388-6981 7052-7364 7527-7659 7698-7943 9535-9659 9671-10133 11759-12221 |
| HYAAH23 | 42 | 1032585 | AL158155 | 1814 | 1-171 2177-2317 2558-3332 3786-4298 4772-6123 6194-6228 6690-7175 7848-8485 8500-9065 9164-9476 9639-9771 9810-10055 11647-11771 11783-12245 13870-14332 |
| HYAAH23 | 42 | 1032585 | AL158156 | 1815 | 1-4481 |
| HYAAH23 | 42 | 1032585 | AL158155 | 1816 | 1-4477 |
| HAJAV28 | 45 | 948630 | AL121579 | 1817 | 1-175 1520-1889 2329-2473 2730-2805 3231-3444 4096-4273 7815-7900 8874-9058 |
| HCE1S21 | 49 | 671209 | AC007666 | 1818 | 1-122 274-371 |

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| HCE1S21 | 49 | 671209 | AC000052 | 1824 | 1-591 2366-2473 |
| HCE1S21 | 49 | 671209 | AC004019 | 1825 | 1-269 324-413 |
| HCE1S21 | 49 | 671209 | AC004019 | 1826 | 1-462 |
| HCE3J64 | 50 | 951228 | AC061705 | 1827 | 1-77 614-729 917-1028 1154-1218 1398-1591 1704-1802 2419-3315 |
| HCFLI54 | 52 | 921382 | AC023278 | 1828 | 1-1977 2006-3504 3802-4090 4113-6041 6143-6242 6252-6919 |

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| HCFLI54 | 52 | 921382 | AC005562 | 1829 | 1-3490 3783-4087 4094-6238 6249-6901 6930-7364 7701-8350 |
| HCFLI54 | 52 | 921382 | AC023278 | 1830 | 1-574 774-1443 |
| HCFLI54 | 52 | 921382 | AC023278 | 1831 | 1-616 |
| HCFLI54 | 52 | 921382 | AC005562 | 1832 | 1-667 |
| HCWDL45 | 55 | 889416 | AC023100 | 1833 | 1-1181 |
| HCWDL45 | 55 | 889416 | Z98747 | 1834 | 1-1181 |
| HDPGQ74 | 59 | 691163 | AC073462 | 1835 | 1-173 1923-2056 2270-2362 4504-5101 5444-5630 6218-6268 8466-8542 8816-8888 10396-10437 |
| HDPGS68 | 60 | 752975 | AC034180 | 1836 | 1-950 |
| HE2FR50 | 64 | 508498 | AC010408 | 1837 | 1-574 1043-1729 1759-1995 2866-3391 3406-3626 3954-4396 4444-4667 5413-5515 8692-8774 8878-9828 13011-13373 14082-14365 15285-16319 |
| HEBGK01 | 67 | 963673 | Z97653 | 1838 | 1-627 815-1256 2165-2714 |
| HEBGK01 | 67 | 963673 | Z97653 | 1839 | 1-146 |
| HEBGK01 | 67 | 963673 | Z97653 | 1840 | 1-487 |
| HEFMB30 | 68 | 691516 | AC016659 | 1841 | 1-862 |
| HEFMB30 | 68 | 691516 | AC012481 | 1842 | 1-862 |
| HEFMB30 | 68 | 691516 | AC016659 | 1843 | 1-447 |
| HEFMB30 | 68 | 691516 | AC012481 | 1844 | 1-447 |
| HEOPE58 | 69 | 851009 | AL078634 | 1845 | 1-40 1089-1226 |

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| HEOPE58 | 69 | 851009 | AL078634 | 1846 | 1-235 3051-3154 3199-3734 |
| HEOPE58 | 69 | 851009 | AL078634 | 1847 | 1-444 |
| HLHDD45 | 75 | 942901 | AC024148 | 1848 | 1-116 629-787 1238-1305 1825-1969 2522-2966 2984-6238 |
| HLHDD45 | 75 | 942901 | AC069253 | 1849 | 1-116 629-787 1238-1305 1824-1968 2521-2965 2983-5879 |
| HLHDD45 | 75 | 942901 | AC044892 | 1850 | 1-116 629-787 1238-1305 1824-1968 2521-2965 2983-6236 |
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| HNHEQ86 | 79 | 785580 | AC024653 | 1853 | 1-731 |
| HSICX21 | 88 | 531267 | AC016333 | 1854 | 1-552 |
| HSICX21 | 88 | 531267 | AC024101 | 1855 | 1-551 |
| HSICX21 | 88 | 531267 | AC016333 | 1856 | 1-448 |
| HSICX21 | 88 | 531267 | AC024101 | 1857 | 1-447 |
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| HSODC08 | 91 | 966264 | AC005332 | 1859 | 1-205 221-693 |
| HSODC08 | 91 | 966264 | AC005332 | 1860 | 1-181 |
| HSQCM85 | 93 | 963554 | AL021918 | 1861 | 1-629 |
| HTOIA82 | 94 | 844319 | AC012446 | 1862 | 1-410 |
| HTOIA82 | 94 | 844319 | AC012446 | 1863 | 1-329 |
| HUUDH57 | 95 | 931155 | AC009073 | 1864 | 1-118 2843-2982 5373-5675 6891-7201 8485-8641 9497-9900 10048-10506 10621-11749 12563-12695 12919-13053 14526-14766 16311-16378 17695-17869 18462-18541 19565-19750 21028-21485 25002-26608 26801-28071 28114-28369 28825-28998 29505-29648 31878-31961 32637-32809 32835-32936 33645-35911 |
| HWAFFW39 | 97 | 947915 | AC008508 | 1865 | 1-124 2706-3000 3745-3882 5914-6036 6110-6413 6491-6844 6912-7681 8888-9020 10437-10570 10686-11022 |
| HWAFFW39 | 97 | 947915 | AC008955 | 1866 | 1-544 2059-2219 2947-3088 5596-5891 |

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| | | | | | 6635-6773 8782-8904 8978-9281 9359-9712 9778-10496 |
| HWAFFW39 | 97 | 947915 | AC008963 | 1867 | 1-124 2645-2940 3685-3822 5831-5953 6027-6330 6408-6761 6828-7597 8806-8938 10353-10487 10603-10939 12315-12471 13563-13693 14450-14528 15001-16291 |
| HWAFFW39 | 97 | 947915 | AC009073 | 1868 | 1-240 2827-3055 4160-4703 6218-6382 7102-7248 9770-10061 10805-10943 12952-13074 13148-13451 13529-13882 13951-14720 15927-16059 17474-17607 17723-18059 19435-19592 20686-20816 21573-21651 22124-23668 24035-24199 24212-24595 24879-25065 25816-26017 26260-26422 26424-26555 26824-27350 27380-27598 27609-27697 29321-29822 30645-30922 |

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| HWAFFW39 | 97 | 947915 | AC009073 | 1869 | 1-452 |
| HWAFFW39 | 97 | 947915 | AC008955 | 1870 | 1-229 |
| HWAFFW39 | 97 | 947915 | AC008963 | 1871 | 1-146 |
| HBGDA14 | 114 | 866258 | AC074220 | 1872 | 1-919 |
| HBGDA14 | 114 | 866258 | AC024580 | 1873 | 1-682 |
| HDPND85 | 119 | 852628 | AC003042 | 1874 | 1-261 1877-2339 3059-3286 3970-4326 4931-5114 6268-6359 7022-7866 7877-8140 8262-8911 |
| HDPND85 | 119 | 852628 | AC003042 | 1875 | 1-754 955-1048 6079-6214 6309-6423 6705-7373 |
| HE9RE21 | 122 | 888243 | AC040908 | 1876 | 1-203 |
| HKABI68 | 125 | 856590 | AC007606 | 1877 | 1-650 |

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| HKABI68 | 125 | 856590 | AC007606 | 1878 | 1-1215 1651-1783 1974-2304 2681-2756 |
| HWHPO29 | 134 | 857383 | AL049779 | 1879 | 1-210 1909-2318 2599-2753 3548-3655 4479-4690 6391-6879 7696-8065 10475-10649 11240-11950 |
| HNTMD81 | 167 | 929511 | AL138795 | 1880 | 1-327 2886-2923 3052-3182 3604-3784 4304-4446 4671-4764 4948-5014 5186-5345 5443-5566 5923-6025 6558-8807 9222-9363 9502-9626 9862-9937 10087-10280 10803-11470 |
| HNTMD81 | 167 | 929511 | AL365403 | 1881 | 1-133 358-451 635-701 873-1032 1130-1253 1610-1712 |

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|---------|-----|--------|----------|------|--|
| | | | | | 2245-2912 |
| HNTMD81 | 167 | 929511 | AL365403 | 1882 | 1-131 |
| HNTMD81 | 167 | 929511 | AL138795 | 1883 | 1-634 |
| HSKCI43 | 169 | 506599 | AC068494 | 1884 | 1-826 |
| HAMFW05 | 230 | 957586 | AC005594 | 1885 | 1-103 2099-2278 2831-3511 4124-4482 6695-6777 7930-8084 8758-8898 9553-9738 10471-10829 11883-12031 12754-12992 13983-14296 14330-14468 14814-14959 15524-15766 17708-17819 18969-19670 20698-22428 |
| HAMFW05 | 230 | 957586 | AC005594 | 1886 | 1-232 |
| HTDAB17 | 249 | 890384 | AC011078 | 1887 | 1-297 359-416 3247-3653 6083-6236 9753-10036 11128-11233 12148-12514 12635-13141 15604-16463 19071-19190 19476-20232 20321-20638 21200-21594 21959-22219 23120-23362 23467-24143 24766-24853 25725-26143 26310-26455 27545-30619 30708-31169 |
| HODGC61 | 277 | 973449 | AC020695 | 1888 | 1-663 |
| HODGC61 | 277 | 973449 | AC017086 | 1889 | 1-663 |
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| HEOQP44 | 315 | 942596 | AC025354 | 1892 | 1-747 |
| HEOQP44 | 315 | 942596 | AL022167 | 1893 | 1-1796 |
| HEOQP44 | 315 | 942596 | AC068470 | 1894 | 1-706 |
| HEOQP44 | 315 | 942596 | AL022344 | 1895 | 1-2022 |
| HEOQP44 | 315 | 942596 | AC006510 | 1896 | 1-1150 |
| HEOQP44 | 315 | 942596 | AC006096 | 1897 | 1-2211 |
| HEOQP44 | 315 | 942596 | AC006106 | 1898 | 1-2215 |
| HEOQP44 | 315 | 942596 | AC006108 | 1899 | 1-2210 |
| HEOQP44 | 315 | 942596 | U82205 | 1900 | 1-2213 |
| HEOQP44 | 315 | 942596 | U82208 | 1901 | 1-2212 |
| HEOQP44 | 315 | 942596 | AC006171 | 1902 | 1-2213 |
| HEOQP44 | 315 | 942596 | AC006177 | 1903 | 1-2212 2216-2455 2951-4547 4559-4639 4902-5697 |
| HEOQP44 | 315 | 942596 | AC006094 | 1904 | 1-1984 |
| HEOQP44 | 315 | 942596 | AC006185 | 1905 | 1-2206 |
| HEOQP44 | 315 | 942596 | AC006184 | 1906 | 1-2204 2208-2447 2943-3574 3724-4540 4552-4633 4896-5715 |
| HEOQP44 | 315 | 942596 | AC006172 | 1907 | 1-2211 |
| HEOQP44 | 315 | 942596 | AC006099 | 1908 | 1-2212 |
| HEOQP44 | 315 | 942596 | AC006103 | 1909 | 1-2213 |
| HEOQP44 | 315 | 942596 | AC006098 | 1910 | 1-2212 |
| HEOQP44 | 315 | 942596 | AC006096 | 1911 | 1-240 737-1362 |
| HEOQP44 | 315 | 942596 | AC006106 | 1912 | 1-240 736-1423 |
| HEOQP44 | 315 | 942596 | AC006108 | 1913 | 1-240 736-1359 |
| HEOQP44 | 315 | 942596 | U82205 | 1914 | 1-255 736-849 1023-1457 |
| HEOQP44 | 315 | 942596 | U82208 | 1915 | 1-240 736-1425 |
| HEOQP44 | 315 | 942596 | AC006171 | 1916 | 1-247 1217-1320 1624-1963 2076-2179 2604-2711 2716-3114 3399-3638 4344-4427 5079-5141 |

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| | | | | | 5439-8153 8268-8798 |
| HEOQP44 | 315 | 942596 | AC006096 | 1917 | 1-110 |
| HEOQP44 | 315 | 942596 | AC006177 | 1918 | 1-67 1558-1614 1692-2134 2610-2767 4075-4344 5072-5484 5971-6837 7042-7752 |
| HEOQP44 | 315 | 942596 | U82205 | 1919 | 1-28 384-522 2412-6373 6598-7151 7230-7525 9388-9464 10003-10111 |
| HEOQP44 | 315 | 942596 | U82208 | 1920 | 1-511 |
| HEOQP44 | 315 | 942596 | AC006171 | 1921 | 1-240 736-1540 7244-8075 8087-8167 |
| HEOQP44 | 315 | 942596 | AC006094 | 1922 | 1-210 |
| HEOQP44 | 315 | 942596 | AC006185 | 1923 | 1-240 736-1359 |
| HEOQP44 | 315 | 942596 | AC006172 | 1924 | 1-240 847-1425 |
| HEOQP44 | 315 | 942596 | AC006184 | 1925 | 1-130 |
| HEOQP44 | 315 | 942596 | AC006099 | 1926 | 1-416 |
| HEOQP44 | 315 | 942596 | AC006099 | 1927 | 1-240 736-1424 |
| HEOQP44 | 315 | 942596 | AC006103 | 1928 | 1-422 |
| HEOQP44 | 315 | 942596 | AC006103 | 1929 | 1-240 737-2325 |
| HEOQP44 | 315 | 942596 | AC006098 | 1930 | 1-291 |
| HEOQP44 | 315 | 942596 | AC006098 | 1931 | 1-240 736-1424 |
| HHEKZ12 | 316 | 878267 | Z81559 | 1932 | 1-1487 |
| HHEKZ12 | 316 | 878267 | AC006186 | 1933 | 1-852 |
| HHEKZ12 | 316 | 878267 | AC016135 | 1934 | 1-845 |
| HHEKZ12 | 316 | 878267 | AL022167 | 1935 | 1-1796 |
| HHEKZ12 | 316 | 878267 | Z81452 | 1936 | 1-2018 2193-2289 5113-6160 |
| HHEKZ12 | 316 | 878267 | AL022344 | 1937 | 1-2022 |
| HHEKZ12 | 316 | 878267 | U82210 | 1938 | 1-851 |
| HHEKZ12 | 316 | 878267 | AC006096 | 1939 | 1-2211 |

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| HHEKZ12 | 316 | 878267 | AC006106 | 1940 | 1-2215 |
| HHEKZ12 | 316 | 878267 | AC006108 | 1941 | 1-2210 |
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| HHEKZ12 | 316 | 878267 | U82208 | 1943 | 1-2212 |
| HHEKZ12 | 316 | 878267 | AC006171 | 1944 | 1-2213 |
| HHEKZ12 | 316 | 878267 | AC006177 | 1945 | 1-2212 2216-2455 2951-4547 4559-4639 4902-5697 |
| HHEKZ12 | 316 | 878267 | AC009260 | 1946 | 1-745 |
| HHEKZ12 | 316 | 878267 | AC006094 | 1947 | 1-1984 |
| HHEKZ12 | 316 | 878267 | AC006179 | 1948 | 1-852 |
| HHEKZ12 | 316 | 878267 | AC006185 | 1949 | 1-2206 |
| HHEKZ12 | 316 | 878267 | AC006184 | 1950 | 1-2204 2208-2447 2943-3574 3724-4540 4552-4633 4896-5715 |
| HHEKZ12 | 316 | 878267 | AC006172 | 1951 | 1-2211 |
| HHEKZ12 | 316 | 878267 | AC006099 | 1952 | 1-2212 |
| HHEKZ12 | 316 | 878267 | AC006103 | 1953 | 1-2213 |
| HHEKZ12 | 316 | 878267 | AC006098 | 1954 | 1-2212 |
| HHEKZ12 | 316 | 878267 | AC006096 | 1955 | 1-240 737-1362 |
| HHEKZ12 | 316 | 878267 | AC006106 | 1956 | 1-240 736-1423 |
| HHEKZ12 | 316 | 878267 | AC006108 | 1957 | 1-240 736-1359 |
| HHEKZ12 | 316 | 878267 | U82205 | 1958 | 1-255 736-849 1023-1457 |
| HHEKZ12 | 316 | 878267 | U82208 | 1959 | 1-240 736-1425 |
| HHEKZ12 | 316 | 878267 | AC006171 | 1960 | 1-247 1217-1320 1624-1963 2076-2179 2604-2711 2716-3114 3399-3638 4344-4427 5079-5141 5439-8153 8268-8798 |
| HHEKZ12 | 316 | 878267 | AC006186 | 1961 | 1-87 |
| HHEKZ12 | 316 | 878267 | U82210 | 1962 | 1-87 |

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| HHEKZ12 | 316 | 878267 | AC006096 | 1963 | 1-110 |
| HHEKZ12 | 316 | 878267 | AC006177 | 1964 | 1-67 1558-1614 1692-2134 2610-2767 4075-4344 5072-5484 5971-6837 7042-7752 |
| HHEKZ12 | 316 | 878267 | U82205 | 1965 | 1-28 384-522 2412-6373 6598-7151 7230-7525 9388-9464 10003-10111 |
| HHEKZ12 | 316 | 878267 | U82208 | 1966 | 1-511 |
| HHEKZ12 | 316 | 878267 | AC006171 | 1967 | 1-240 736-1540 7244-8075 8087-8167 |
| HHEKZ12 | 316 | 878267 | AC009260 | 1968 | 1-87 |
| HHEKZ12 | 316 | 878267 | AC006094 | 1969 | 1-210 |
| HHEKZ12 | 316 | 878267 | AC006179 | 1970 | 1-87 |
| HHEKZ12 | 316 | 878267 | AC006185 | 1971 | 1-240 736-1359 |
| HHEKZ12 | 316 | 878267 | AC006172 | 1972 | 1-240 847-1425 |
| HHEKZ12 | 316 | 878267 | AC006184 | 1973 | 1-130 |
| HHEKZ12 | 316 | 878267 | AC006099 | 1974 | 1-416 |
| HHEKZ12 | 316 | 878267 | AC006099 | 1975 | 1-240 736-1424 |
| HHEKZ12 | 316 | 878267 | AC006103 | 1976 | 1-422 |
| HHEKZ12 | 316 | 878267 | AC006103 | 1977 | 1-240 737-2325 |
| HHEKZ12 | 316 | 878267 | AC006098 | 1978 | 1-291 |
| HHEKZ12 | 316 | 878267 | AC006098 | 1979 | 1-240 736-1424 |
| HHELA35 | 317 | 878217 | Z81559 | 1980 | 1-1487 |
| HHELA35 | 317 | 878217 | AC006186 | 1981 | 1-852 |
| HHELA35 | 317 | 878217 | AC016135 | 1982 | 1-845 |
| HHELA35 | 317 | 878217 | AC022305 | 1983 | 1-878 |
| HHELA35 | 317 | 878217 | AL022167 | 1984 | 1-1796 |
| HHELA35 | 317 | 878217 | Z81452 | 1985 | 1-2018 2193-2289 5113-6160 |
| HHELA35 | 317 | 878217 | AL022344 | 1986 | 1-2022 |
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| HHELA35 | 317 | 878217 | AC006106 | 1989 | 1-2215 |
| HHELA35 | 317 | 878217 | AC006108 | 1990 | 1-2210 |
| HHELA35 | 317 | 878217 | U82205 | 1991 | 1-2213 |
| HHELA35 | 317 | 878217 | U82208 | 1992 | 1-2212 |
| HHELA35 | 317 | 878217 | AC006171 | 1993 | 1-2213 |
| HHELA35 | 317 | 878217 | AC006177 | 1994 | 1-2212 2216-2455 2951-4547 4559-4639 4902-5697 |
| HHELA35 | 317 | 878217 | AC009260 | 1995 | 1-745 |
| HHELA35 | 317 | 878217 | AC006094 | 1996 | 1-1984 |
| HHELA35 | 317 | 878217 | AC006179 | 1997 | 1-852 |
| HHELA35 | 317 | 878217 | AC006185 | 1998 | 1-2206 |
| HHELA35 | 317 | 878217 | AC006184 | 1999 | 1-2204 2208-2447 2943-3574 3724-4540 4552-4633 4896-5715 |
| HHELA35 | 317 | 878217 | AC006172 | 2000 | 1-2211 |
| HHELA35 | 317 | 878217 | AC006099 | 2001 | 1-2212 |
| HHELA35 | 317 | 878217 | AC006103 | 2002 | 1-2213 |
| HHELA35 | 317 | 878217 | AC006098 | 2003 | 1-2212 |
| HHELA35 | 317 | 878217 | AC006096 | 2004 | 1-240 737-1362 |
| HHELA35 | 317 | 878217 | AC006106 | 2005 | 1-240 736-1423 |
| HHELA35 | 317 | 878217 | AC006108 | 2006 | 1-240 736-1359 |
| HHELA35 | 317 | 878217 | U82205 | 2007 | 1-255 736-849 1023-1457 |
| HHELA35 | 317 | 878217 | U82208 | 2008 | 1-240 736-1425 |
| HHELA35 | 317 | 878217 | AC006171 | 2009 | 1-247 1217-1320 1624-1963 2076-2179 2604-2711 2716-3114 3399-3638 4344-4427 5079-5141 5439-8153 8268-8798 |
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| HHELA35 | 317 | 878217 | U82210 | 2011 | 1-87 |
| HHELA35 | 317 | 878217 | AC006096 | 2012 | 1-110 |
| HHELA35 | 317 | 878217 | AC006177 | 2013 | 1-67 1558-1614 1692-2134 2610-2767 4075-4344 5072-5484 5971-6837 7042-7752 |
| HHELA35 | 317 | 878217 | U82205 | 2014 | 1-28 384-522 2412-6373 6598-7151 7230-7525 9388-9464 10003-10111 |
| HHELA35 | 317 | 878217 | U82208 | 2015 | 1-511 |
| HHELA35 | 317 | 878217 | AC006171 | 2016 | 1-240 736-1540 7244-8075 8087-8167 |
| HHELA35 | 317 | 878217 | AC009260 | 2017 | 1-87 |
| HHELA35 | 317 | 878217 | AC006094 | 2018 | 1-210 |
| HHELA35 | 317 | 878217 | AC006179 | 2019 | 1-87 |
| HHELA35 | 317 | 878217 | AC006185 | 2020 | 1-240 736-1359 |
| HHELA35 | 317 | 878217 | AC006172 | 2021 | 1-240 847-1425 |
| HHELA35 | 317 | 878217 | AC006184 | 2022 | 1-130 |
| HHELA35 | 317 | 878217 | AC006099 | 2023 | 1-416 |
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| HMUBI13 | 488 | 937820 | AC012180 | 2197 | 1-101 |
| HAFAH26 | 490 | 940254 | AL353192 | 2198 | 1-1723 1892-5060 |
| HAFAH26 | 490 | 940254 | AC013708 | 2199 | 1-1723 1888-5062 |
| HAFAH26 | 490 | 940254 | AL354985 | 2200 | 1-1723 1888-5061 |
| HAFAH26 | 490 | 940254 | AL157762 | 2201 | 1-1724 1889-5063 |
| HAFAH26 | 490 | 940254 | AC013708 | 2202 | 1-297 |
| HAFAH26 | 490 | 940254 | AL354985 | 2203 | 1-297 |
| HAFAH26 | 490 | 940254 | AC013708 | 2204 | 1-366 |
| HAFAH26 | 490 | 940254 | AL157762 | 2205 | 1-366 |

| | | | | | |
|---------|-----|--------|----------|------|---|
| HAFAH26 | 490 | 940254 | AL157762 | 2206 | 1-297 |
| HDPJH11 | 497 | 951371 | AC024667 | 2207 | 1-93 4325-4485 8156-8260 9251-9460 |
| HDPJH11 | 497 | 951371 | AC024667 | 2208 | 1-436 |
| HWADY95 | 501 | 951731 | AC068426 | 2209 | 1-103 1135-1280 2068-2219 2711-2816 2838-3235 3559-4903 |
| HWADY95 | 501 | 951731 | AC012467 | 2210 | 1-765 1429-1580 2293-2424 3456-3601 4389-4540 5032-5137 5159-5556 5880-7210 |
| HWADY95 | 501 | 951731 | AC012467 | 2211 | 1-344 |
| HWADY95 | 501 | 951731 | AC012467 | 2212 | 1-555 |
| HPCRA07 | 503 | 952124 | AC015936 | 2213 | 1-540 1047-1330 1887-3313 3648-3758 3868-4165 4348-4516 4828-5035 5234-5330 5455-6124 6208-6297 6493-6624 6860-6943 |
| HADFD82 | 506 | 953295 | AL022328 | 2214 | 1-481 729-828 1094-1193 1289-1396 1553-1617 1798-1929 2089-2152 2247-4100 4146-4381 4518-4577 4865-4961 5157-5580 5725-6072 |
| HADFD82 | 506 | 953295 | AL022328 | 2215 | 1-723 |

| | | | | | |
|---------|-----|--------|----------|------|---|
| HADFD82 | 506 | 953295 | AL022328 | 2216 | 1-81 162-241 315-880 1024-1324 1365-1937 2215-2794 |
| HLTCU08 | 514 | 960951 | AL359452 | 2217 | 1-1504 |
| HLTCU08 | 514 | 960951 | AC005500 | 2218 | 1-3341 |
| HLTCU08 | 514 | 960951 | AC007731 | 2219 | 1-3341 |
| HLTCU08 | 514 | 960951 | AC005500 | 2220 | 1-923 4251-5635 6031-6618 6898-8078 |
| HLTCU08 | 514 | 960951 | AC005500 | 2221 | 1-411 |
| HLTCU08 | 514 | 960951 | AC007731 | 2222 | 1-923 4251-5635 6031-6618 6898-8078 |
| HLTCU08 | 514 | 960951 | AC007731 | 2223 | 1-411 |
| HTKAA03 | 516 | 961002 | AC073152 | 2224 | 1-465 |
| HTKAA03 | 516 | 961002 | AC073152 | 2225 | 1-638 |
| HMSGF27 | 517 | 962420 | AL356652 | 2226 | 1-191 227-519 2321-2362 2983-3223 4301-4435 4863-4968 7663-7820 7975-8116 8579-8760 8826-9095 9333-9460 11514-11621 12209-12595 |
| HMSGF27 | 517 | 962420 | AL356652 | 2227 | 1-264 |
| HMSGF27 | 517 | 962420 | AL356652 | 2228 | 1-659 |
| HE2SB11 | 521 | 965611 | AL139082 | 2229 | 1-428 2627-2696 3808-9516 |
| HE2SB11 | 521 | 965611 | AL139082 | 2230 | 1-423 |
| HE2SB11 | 521 | 965611 | AL139082 | 2231 | 1-378 |
| HLICJ19 | 523 | 966969 | AL139317 | 2232 | 1-32 2015-2578 2609-3255 3589-3628 4619-5174 6796-6965 7977-8037 |

| | | | | | |
|---------|-----|--------|----------|------|---|
| | | | | | 9549-9719 10720-10781 11892-11984 13002-16279 |
| HLICJ19 | 523 | 966969 | AL139317 | 2233 | 1-1541 |
| HHEKP47 | 527 | 974402 | AC023609 | 2234 | 1-304 |
| HHEKP47 | 527 | 974402 | AC074220 | 2235 | 1-238 |
| HHEKP47 | 527 | 974402 | AC023609 | 2236 | 1-529 |
| HHEKP47 | 527 | 974402 | AC074220 | 2237 | 1-367 |
| HCEOX38 | 531 | 881200 | AC005973 | 2238 | 1-221 228-420 636-800 1154-1400 1833-1916 2335-2450 2659-2749 2892-4525 4674-4925 5019-5177 5375-5547 5684-5785 5873-6024 6108-6270 6345-6660 6692-7868 |
| HCEOX38 | 531 | 881200 | AC005973 | 2239 | 1-562 570-740 801-1004 |
| HCEOX38 | 531 | 881200 | AC005973 | 2240 | 1-68 328-494 1925-2023 |
| HPDVO67 | 533 | 911405 | AC005954 | 2241 | 1-118 1208-1596 5809-5862 8096-8208 8442-8680 10094-10308 10499-10599 10960-11170 11298-11645 12507-12838 13149-13818 13929-14078 15553-15626 16027-16241 16318-16421 17336-17629 17807-18015 |

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|---------|-----|--------|----------|------|--|
| | | | | | 18421-19058 19159-19221 19233-19928 20115-20644 20731-21386 22053-22267 22362-22535 22645-22988 23309-23476 23569-23649 23739-23886 24169-24295 25772-25881 25999-26204 27159-27504 27519-27621 28747-29313 29474-29846 30160-30276 31078-31168 |
| HPDVO67 | 533 | 911405 | AC005954 | 2242 | 1-131 |
| HFXCU55 | 537 | 499457 | AC034243 | 2243 | 1-641 |
| HFXCU55 | 537 | 499457 | AC020758 | 2244 | 1-587 |
| HFXCU55 | 537 | 499457 | AC020758 | 2245 | 1-65 72-459 633-1391 1401-1505 3814-3915 4909-5189 5410-6542 9420-9967 10046-10185 10271-10646 |
| HCEBMS1 | 541 | 536558 | AC007326 | 2246 | 1-472 4950-5163 9929-10114 10431-10462 10950-11102 11348-11731 11834-11960 12266-12401 12974-13036 13215-13335 13748-13826 14441-15128 15278-15810 15951-16445 16552-16701 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 17658-17839 17949-18318 18325-18679 19157-19768 20570-20920 21264-21605 22617-22714 22788-23458 |
| HCEBM51 | 541 | 536558 | AC008103 | 2247 | 1-472 4950-5163 9929-10114 10431-10462 10950-11102 11348-11731 11834-11976 12265-12400 12973-13035 13214-13334 13747-13825 14440-15127 15277-15809 15950-16444 16551-16700 17657-17838 17948-18317 18324-18678 19156-19767 20569-20919 21263-21604 22616-22713 22787-23457 |
| HCEBM51 | 541 | 536558 | AC007325 | 2248 | 1-472 4950-5163 9929-10114 10431-10462 10950-11102 11348-11731 11834-11978 12266-12401 12974-13036 13215-13335 13748-13826 14442-15129 15279-15811 15952-16446 16553-16702 17659-17840 17950-18674 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 19152-19763 20565-20915 21259-21600 22611-22708 22782-23452 |
| HCEBM51 | 541 | 536558 | AC007326 | 2249 | 1-556 1064-2403 2424-3605 3819-4142 4155-4274 4702-5531 5609-5785 |
| HCEBM51 | 541 | 536558 | AC007326 | 2250 | 1-164 |
| HCEBM51 | 541 | 536558 | AC008103 | 2251 | 1-556 1064-2403 2424-3605 3819-4142 4155-4274 4702-5531 5612-5785 |
| HCEBM51 | 541 | 536558 | AC008103 | 2252 | 1-164 |
| HCEBM51 | 541 | 536558 | AC007325 | 2253 | 1-556 1098-2437 2458-3639 3853-4176 4189-4308 4736-5565 5643-5819 |
| HCEBM51 | 541 | 536558 | AC007325 | 2254 | 1-164 |
| HNHHW82 | 545 | 684342 | AC074221 | 2255 | 1-160 |
| HNHHW82 | 545 | 684342 | AC020818 | 2256 | 1-709 |
| HNHHW82 | 545 | 684342 | AC020884 | 2257 | 1-709 |
| HNHHW82 | 545 | 684342 | AC074221 | 2258 | 1-408 |
| HHFFG80 | 547 | 733387 | AL135799 | 2259 | 1-127 1085-1228 1371-1531 1548-2225 2375-2593 3502-4133 4212-4554 4757-7640 |
| HHFFG80 | 547 | 733387 | AL135928 | 2260 | 1-127 1085-1228 1371-1531 1548-2225 2375-2593 3502-4133 4212-4554 |

| | | | | | |
|---------|-----|--------|----------|------|---|
| | | | | | 4757-7640 |
| HHFFG80 | 547 | 733387 | AL357556 | 2261 | 1-125 1370-1532 2542-2592 4216-4558 4948-5554 |
| HHFFG80 | 547 | 733387 | AC025395 | 2262 | 1-127 1085-1228 1371-1531 1548-2225 2375-2593 3503-4135 4215-4557 4760-8240 |
| HHFFG80 | 547 | 733387 | AL357556 | 2263 | 1-760 1068-1270 1409-2384 |
| HSDKI89 | 551 | 786812 | AC012620 | 2264 | 1-525 |
| HLDQU68 | 553 | 825558 | U95090 | 2265 | 1-160 239-402 3754-3867 3888-4257 4312-5026 6123-6276 6565-6847 |
| HLDQU68 | 553 | 825558 | U95090 | 2266 | 1-315 |
| HLDQU68 | 553 | 825558 | U95090 | 2267 | 1-142 |
| HTXOH20 | 555 | 837509 | AC013591 | 2268 | 1-97 2761-2844 4015-4414 8029-8100 9115-9571 10597-10742 10954-11043 11799-12484 12669-13256 13507-13594 13993-14102 14709-14853 15126-15192 15452-15534 16964-17513 17846-17960 18303-18418 18672-20097 |
| HTXOH20 | 555 | 837509 | AC013591 | 2269 | 1-110 921-1200 |
| HSLFG13 | 556 | 847314 | AC008792 | 2270 | 1-711 |

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|---------|-----|--------|----------|------|---|
| HSDAI07 | 559 | 859237 | AC034099 | 2271 | 1-826 |
| HSLDO63 | 562 | 866332 | AC074219 | 2272 | 1-523 |
| HSLDO63 | 562 | 866332 | AC074219 | 2273 | 1-512 |
| HNHAG26 | 563 | 866694 | AC074220 | 2274 | 1-839 |
| HNHAG26 | 563 | 866694 | AC073351 | 2275 | 1-365 |
| HEBCK42 | 566 | 875541 | AC067749 | 2276 | 1-49 598-1355 1972-2268 |
| HEBCK42 | 566 | 875541 | AC067966 | 2277 | 1-758 |
| HEBCK42 | 566 | 875541 | AL355138 | 2278 | 1-49 598-1355 1974-2270 |
| HEBCK42 | 566 | 875541 | AL355138 | 2279 | 1-399 |
| HEBCK42 | 566 | 875541 | AC067749 | 2280 | 1-399 |
| HFIJE03 | 572 | 914882 | AC026265 | 2281 | 1-141 |
| HFIJE03 | 572 | 914882 | AP001893 | 2282 | 1-190 581-749 1831-2145 2181-2629 2713-3611 3960-4537 5661-5948 6024-6171 6801-7034 7311-7405 7979-9544 |
| HFIJE03 | 572 | 914882 | AP000717 | 2283 | 1-301 351-799 883-1782 2131-2708 3832-4119 4195-4342 4972-5205 5482-5576 6150-7715 |
| HFIJE03 | 572 | 914882 | AC011728 | 2284 | 1-301 351-799 883-1781 2130-2707 3831-4118 4194-4341 4971-5204 5481-5575 6149-7712 |
| HTHDJ23 | 577 | 921274 | AC068620 | 2285 | 1-2395 3653-3776 4371-4418 |
| HTHDJ23 | 577 | 921274 | AC068620 | 2286 | 1-733 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| HSQFX64 | 579 | 922581 | AL049697 | 2287 | 1-1216 1879-2223 4381-4541 5424-5808 7119-7260 10651-10772 13801-13860 15071-15143 15616-15917 16189-17858 18042-18076 18423-18519 18638-19174 19787-20084 20299-20367 20825-21387 |
| HSQFX64 | 579 | 922581 | AL049697 | 2288 | 1-228 |
| HSQFX64 | 579 | 922581 | AL049697 | 2289 | 1-107 |
| HEGAU68 | 588 | 950009 | AC060820 | 2290 | 1-27 124-298 385-448 538-663 773-809 1010-1129 1442-1518 1636-1727 1855-1975 2263-2396 2492-2710 2875-4213 4346-4516 4572-6197 6278-6508 6762-7406 7537-7963 8181-8292 8539-8721 9815-9994 10264-10401 |
| HEGAU68 | 588 | 950009 | AC068946 | 2291 | 1-27 125-299 386-449 539-664 774-810 1011-1130 1443-1519 1637-1728 1856-1974 |

| | | | | | |
|---------|-----|--------|----------|------|---|
| | | | | | 2262-2395 2491-2709 2874-4212 4345-4515 4571-6197 6278-6501 7596-7957 8177-8265 |
| HEGAU68 | 588 | 950009 | AC060820 | 2292 | 1-145 |
| HEGAU68 | 588 | 950009 | AC068946 | 2293 | 1-238 |
| HEGAU68 | 588 | 950009 | AC068946 | 2294 | 1-145 |
| HNGKH38 | 589 | 951032 | AC019122 | 2295 | 1-439 1012-1359 1441-1505 2435-2624 2884-3145 3411-3503 3682-5647 |
| HNGKH38 | 589 | 951032 | AC019122 | 2296 | 1-314 |
| HNGKH38 | 589 | 951032 | AC019122 | 2297 | 1-333 |
| HNHNN26 | 590 | 952398 | AC078913 | 2298 | 1-591 |
| HNHNN26 | 590 | 952398 | AC010357 | 2299 | 1-577 |
| HNHNN26 | 590 | 952398 | AC074334 | 2300 | 1-576 |
| HNHNN26 | 590 | 952398 | AC074334 | 2301 | 1-283 |
| HSLHV08 | 594 | 958582 | AC074221 | 2302 | 1-741 |
| HSLHV08 | 594 | 958582 | AC055703 | 2303 | 1-536 |
| HSLHV08 | 594 | 958582 | AC022123 | 2304 | 1-209 284-376 407-598 |
| HSLHV08 | 594 | 958582 | AC074220 | 2305 | 1-741 |
| HSLHV08 | 594 | 958582 | AC074220 | 2306 | 1-610 |
| HBGMN45 | 603 | 967744 | AC022123 | 2307 | 1-249 484-1169 |
| HSDKF67 | 607 | 933059 | AC020885 | 2308 | 1-616 |
| HCEPH84 | 614 | 910864 | AC013603 | 2309 | 1-302 692-1498 2237-2673 5316-5528 6508-7733 |
| HNFD052 | 615 | 916260 | AC012307 | 2310 | 1-1998 |
| HWLLR80 | 622 | 931564 | AL139349 | 2311 | 1-172 4417-4509 4927-5011 6749-6896 8625-8845 8932-10907 10985-11137 12855-12935 |

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|---------|-----|--------|----------|------|--|
| | | | | | 13320-13649 18210-18567 18714-18992 19154-19277 19328-19828 20293-20517 20709-21710 |
| HWLLR80 | 622 | 931564 | AL139349 | 2312 | 1-208 |
| HSYDB42 | 646 | 933545 | AL022318 | 2313 | 1-156 1369-1531 1988-2167 2802-3008 3540-3823 4045-6131 |
| HSYDB42 | 646 | 933545 | AL022318 | 2314 | 1-492 |
| HSYDB42 | 646 | 933545 | AL022318 | 2315 | 1-407 1173-1467 1693-1857 |
| HBGSS51 | 651 | 954855 | AC012615 | 2316 | 1-607 763-1910 2291-2402 2983-3588 4170-4242 |
| HBGSS51 | 651 | 954855 | AC012615 | 2317 | 1-451 |
| HBGSS51 | 651 | 954855 | AC012615 | 2318 | 1-2083 2996-3117 3196-3330 3338-3638 3847-4160 4362-4596 5559-6225 6740-7087 7196-7297 7410-7746 7903-8059 8362-8495 8982-9518 10231-10522 11163-11210 |

[50] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

TABLE 2

| Clone ID NO:Z | Contig ID: | SEQ ID NO:X | Analysis Method | PFam/NR Description | PFam/NR Accession Number | Score/ Percent Identity | NT From | NT To |
|------------------|---------------|-------------------|--------------------|--|---|-------------------------------|------------|-------------|
| HHMMC14 | 1152250 | 11 | blastx.2 | GLYOXYLATE REDUCTASE (EC 1.1.1.79). | sp Q9UBQ7 Q9UBQ 7 | 96% | 105 | 1088 |
| HHMMC14 | 969371 | 652 | HMMER 1.8 | PFAM: D-isomer specific 2-hydroxyacid dehydrogenases | PF00389 | 217.83 | 336 | 965 |
| HSLEQ79 | 1184946 | 12 | blastx.14 | (AF146018) hydroxypyruvate reductase [Homo sapiens] | gi 5639830 gb AAD4 5886.1 AF146018_1 | 96% | 87 | 1070 |
| HSLEQ79 | 1184946 | 12 | blastx.2 | D-lactate dehydrogenase (EC 1.1.1.28) - Escherichia coli | pir G64888 G64888 | 93% | 674 | 156 |
| HSLEQ79 | 752382 | 653 | HMMER 2.1.1 | PFAM: D-isomer specific 2-hydroxyacid dehydrogenases | PF00389 | 222 | 19 | 453 |
| HUCME08 | 1082023 | 13 | blastx.2 | GLYOXYLATE REDUCTASE (EC 1.1.1.79). | sp Q9UBQ7 Q9UBQ 7 | 88% 100% | 110 54 | 625 107 |
| HUCME08 | 868780 | 654 | HMMER 2.1.1 | PFAM: D-isomer specific 2-hydroxyacid dehydrogenases | PF00389 | 93.4 | 275 | 556 |
| HNGOW33 | 1152254 | 14 | blastx.2 | 8-amino-7-oxononanoate synthase (EC 2.3.1.47) - Escherichia coli | pir D32025 SYBCKP | 91% 70% | 547 336 | 1158 497 |

| | | | | | | | | |
|---------|---------|-----|----------------|--|-------------------------------|---------------------|-------------------|-------------------|
| HNGOW33 | 957351 | 655 | HMMER 2.1.1 | PFAM: Aminotransferases class-II (AE000195) orf, hypothetical protein [Escherichia coli] | PF00222 | 441.9 | 409 | 1251 |
| | | | blastx.14 | | gi 1787167 gb AAC7 4022.1 | 99% | 2714 | 3712 |
| HT4GD03 | 1103896 | 15 | blastx.2 | 2-AMINO-3- KETOBUTYRATE COENZYME A LIGASE, MITOCHONDRIAL 1 | sp O75600 KBL_HU MAN | 93% 100% | 153 89 | 968 166 |
| HT4GD03 | 923731 | 656 | HMMER 1.8 | PFAM: Aminotransferases class-II | PF00222 | 78.93 | 575 | 877 |
| | | | blastx.14 | d 466N1.2 (2-amino-3- ketobutyrate-CoA ligase mRNA, 1 | gi 4808241 emb CAB 42830.1 | 100% 87% 100% | 584 153 140 | 967 569 166 |
| HAQBZ89 | 949061 | 16 | HMMER 1.8 | PFAM: Aminotransferases class- III pyridoxal-phosphate | PF00202 | 62.49 | 68 | 325 |
| | | | blastx.2 | CG8745 PROTEIN. | sp Q9VU95 Q9VU95 | 52% | 8 | 316 |
| HCCCC81 | 949062 | 17 | HMMER 1.8 | PFAM: Aminotransferases class- III pyridoxal-phosphate | PF00202 | 178.37 | 187 | 816 |
| | | | blastx.2 | hypothetical protein T01B11.2 - Caenorhabditis elegans | pir T25848 T25848 | 46% | 190 | 879 |
| HE8PW83 | 927532 | 18 | HMMER 1.8 | PFAM: Aminotransferases class- III pyridoxal-phosphate | PF00202 | 139.27 | 4 | 465 |
| | | | blastx.2 | ALANINE-- GLYOXYLATE AMINOTRANSFERASE | sp Q64565 AGT2_R AT | 83% | 4 | 546 |

| | | | | | | | | |
|---------|---------|-----|----------------|---|------------------------------|-------------------|-----------------|---------------------|
| HE9QQ22 | 949080 | 19 | HMMER 2.1.1 | 2 PRECURSOR (EC 1.1 PFAM: Aminotransferases class- III pyridoxal-phosphate | PF00202 | 105.1 | 285 | 545 |
| | | | blastx.2 | ALANINE-- GLYOXYLATE AMINOTRANSFERASE | sp Q64565 AGT2_R AT | 51% 43% 49% | 3 545 682 | 1070 1003 999 |
| HFPEB39 | 946170 | 20 | HMMER 1.8 | 2 PRECURSOR (EC 1.1 PFAM: Aminotransferases class- III pyridoxal-phosphate | PF00202 | 235.05 | 1613 | 714 |
| | | | blastx.2 | hypothetical protein T01B11.2 - Caenorhabditis elegans | pir T25848 T25848 | 49% | 1613 | 651 |
| HSDJI44 | 1151680 | 21 | blastx.2 | adenosylmethionine--8- amino-7-oxononanoate transaminase (EC 2.6.1.62) - Escherichia coli | pir F64813 XNECDP | 96% | 857 | 2143 |
| HSDJI44 | 974784 | 657 | HMMER 2.1.1 | PFAM: Aminotransferases class- III pyridoxal-phosphate | PF00202 | 511.4 | 894 | 1835 |
| | | | blastx.14 | (AE000180) 7,8- diaminopelargonic acid synthetase [Escherichia coli] | gi 1786991 gb AAC7 3861.1 | 99% 100% | 795 1837 | 1841 1860 |
| HE9DG38 | 1181748 | 22 | blastx.2 | Putative selenocysteine lyase. | sp AAF36816 AAF36 816 | 99% | 44 | 994 |
| HE9DG38 | 943384 | 658 | HMMER 2.1.1 | PFAM: Aminotransferases class- | PF00266 | 215.1 | 160 | 1326 |

| | | | | | | | | | | | |
|---------|---------|-----|--|--|----------------|-----------|--|------------------------------|---|--|---|
| | | | | | V | blastx.14 | similar to NIFS protein (nitrogen fixation) [Caenorhabditis elegans] | gi 722379 gb AAC46 685.1 | 45% 53% 61% 46% 41% 57% 41% | 442 877 724 1210 1081 313 1379 | 678 1038 840 1344 1209 375 1450 |
| HGBAT24 | 1024746 | 23 | | | blastx.2 | | phosphoserine transaminase (EC 2.6.1.52) - Escherichia coli | pir B64830 B64830 | 97% | 1 | 369 |
| HGBAT24 | 761143 | 659 | | | HMMER 2.1.1 | | PFAM: Aminotransferases class- V | PF00266 | 128.3 | 10 | 369 |
| HTDAF92 | 1181747 | 24 | | | blastx.2 | | CDNA FLJ10515 FIS, CLONE NT2RP2000764, WEAKLY SIMILAR TO I | sp BAA91659 BAA9 1659 | 100% | 256 | 1011 |
| HTDAF92 | 943385 | 660 | | | HMMER 2.1.1 | | PFAM: Aminotransferases class- V | PF00266 | 104.6 | 163 | 597 |
| | | | | | blastx.2 | | (AF175767) putative selenocysteine lyase [Homo I | gb AAF36816.1 AF1 75767_1 | 100% | 160 | 627 |
| HAPSI19 | 668405 | 25 | | | HMMER 1.8 | | PFAM: Cytochrome C and Quinol oxidase polypeptide I | PF00115 | 75.81 | 263 | 382 |
| | | | | | blastx.2 | | cytochrome-c oxidase (EC 1.9.3.1) chain I - human | pir A00463 ODHU1 | 76% 95% | 3 263 | 263 382 |

| | | | | | | | | |
|---------|---------|-----|-----------------------------|---|---|-----------------------------|---------------------------|----------------------------|
| HADTU18 | 666268 | 26 | HMMER 1.8 blastx.2 | mitochondrion PFAM: Cytochrome C oxidase subunit II cytochrome-c oxidase (EC 1.9.3.1) chain II - human mitochondrion | PF00116 pir A00472 OBHU2 | 50% 100% 99.8 | 28 385 185 | 87 399 307 |
| HNTEF53 | 954852 | 27 | HMMER 1.8 blastx.2 | PFAM: Cytochrome P450 prostaglandin omega- hydroxylase (EC 1.14.15.-) cytochrome 1 | PF00067 pir S32315 A29368 | 102.61 49% 42% 60% | 369 821 279 1705 | 887 1714 902 1749 |
| HWLLB11 | 954849 | 28 | HMMER 1.8 blastx.2 | PFAM: Cytochrome P450 CYTOCHROME P450 4C3 (EC 1.14.14.1) (CYP1VC3). | PF00067 sp Q9VA27 Q9VA27 | 159.13 46% 44% | 75 78 4 | 506 512 75 |
| HCRQK86 | 1193068 | 29 | blastx.2 | PROTEIN PHOSPHATASE 2C. | sp Q9Z1Z6 Q9Z1Z6 | 95% | 164 | 1339 |
| HCRQK86 | 918014 | 662 | HMMER 2.1.1 blastx.14 | PFAM: Protein phosphatase 2C (AF095927) protein phosphatase 2C [Rattus norvegicus] | PF00481 gi 3777604 gb AAC9 7497.1 | 248.4 89% | 467 149 | 1297 1324 |
| HOCOT88 | 933635 | 30 | HMMER 2.1.1 blastx.2 | PFAM: Protein phosphatase 2C protein phosphatase 2C- like protein - Arabidopsis thaliana | PF00481 pir T50783 T50783 | 196.9 38% | 643 619 | 1350 1371 |
| HELEF11 | 926930 | 31 | HMMER | PFAM: Pyridoxal- | PF00282 | 202.9 | 146 | 565 |

[illegible]

| | | | | | PHOSPHOLIPASE C (FRAGMENT). | | | | | |
|---------|---------|-----|-----------------------------|--|--|------------------------------|------------|------------|------------|--|
| HUFDB74 | 901451 | 664 | HMMER 2.1.1 | | PFAM: Phosphatidylinositol- specific phospholipase C, Y domain | PF00387 | 89.4 | 2 | 127 | |
| HBXAB33 | 1229908 | 36 | blastx.2 | | growth/differentiation factor 5 - human | pir JC2347 JC2347 | 98% | 54 | 581 | |
| HBXAB33 | 957228 | 665 | HMMER 2.1.1 blastx.14 | | PFAM: Aminotransferases class-I aspartate aminotransferase precursor (2.6.1.1) [Homo sapiens] | PF00155 | 663.4 | 2286 | 1081 | |
| HMABF84 | 1198479 | 37 | blastx.2 | | 1- AMINOCYCLOPROPAN E-CARBOXYLATE SYNTHASE. | gi 179104 gb AAA35 568.1 | 95% | 2370 | 1081 | |
| HMABF84 | 944629 | 666 | HMMER 1.8 blastx.14 | | PFAM: Aminotransferases class-I (AF108420) 1- aminocyclopropane- carboxylate synthase [Fugu rubripes] | sp Q9W698 Q9W698 | 54% | 770 | 1462 | |
| HPTVF17 | 1150836 | 38 | blastx.2 | | 1- AMINOCYCLOPROPAN E-CARBOXYLATE SYNTHASE. | PF00155 | 37.62 | 55 | 429 | |
| HPTVF17 | 936688 | 667 | HMMER 1.8 blastx.2 | | PFAM: Aminotransferases class-I (AF108420) 1- aminocyclopropane- carboxylate synthase [Fugu rubripes] | gi 4426837 gb AAD2 0564.1 | 58% 43% | 1 452 | 447 499 | |
| HPTVF17 | 936688 | 667 | HMMER 1.8 blastx.2 | | PFAM: Aminotransferases class-I (AF108420) 1- aminocyclopropane- carboxylate synthase [Fugu rubripes] | sp Q9W698 Q9W698 | 57% 59% | 188 574 | 565 759 | |
| HPTVF17 | 936688 | 667 | HMMER 1.8 blastx.2 | | PFAM: Aminotransferases class-I (AF108420) 1- aminocyclopropane- carboxylate synthase [Fugu rubripes] | PF00155 | 37.58 | 275 | 607 | |
| HPTVF17 | 936688 | 667 | HMMER 1.8 blastx.2 | | PFAM: Aminotransferases class-I (AF108420) 1- aminocyclopropane- carboxylate synthase [Fugu rubripes] | gb AAD20564.1 | 52% | 188 | 679 | |

| | | | | | | | | | |
|---------|---------|-----|--|----------------|--|-------------------------------|------------|----------|------------|
| HSDIC55 | 1197407 | 39 | | blastx.2 | aminoacylpropane- carboxylate synthase [Fugu rubripes] | pir A00598 XNECD | 96% | 115 | 345 |
| HSDIC55 | 506582 | 668 | | HMMER 1.8 | PFAM: Aminotransferases class-I | PF00155 | 97.17 | 106 | 363 |
| HSDIL35 | 1228138 | 40 | | blastx.2 | aspartate transaminase (EC 2.6.1.1) - Escherichia coli | pir A00598 XNECD | 98% | 2 | 226 |
| HSDIL35 | 656370 | 669 | | HMMER 2.1.1 | PFAM: Aminotransferases class-I | PF00155 | 195.1 | 3 | 371 |
| HTXSM05 | 1104951 | 41 | | blastx.2 | alanine transaminase (EC 2.6.1.2), cytosolic - human | pir A040465 A040465 | 67% 70% | 5 456 | 406 515 |
| HTXSM05 | 958447 | 670 | | HMMER 1.8 | PFAM: Aminotransferases class-I | PF00155 | 38.39 | 23 | 316 |
| | | | | blastx.14 | alanine aminotransferase [Homo sapiens] | gi 1507680 dbj BAA0 1186.1 | 66% | 5 | 358 |
| HYAAH23 | 1032585 | 42 | | blastx.2 | GLYOXYLATE REDUCTASE (EC 1.1.1.79) | sp Q9UBQ7 Q9UBQ 7 | 92% | 1 | 606 |
| HTPDX13 | 1134372 | 43 | | blastx.2 | CARBOXYPEPTIDASE X2. | sp O54860 O54860 | 88% | 2 | 922 |
| HTPDX13 | 948419 | 671 | | HMMER 1.8 | PFAM: Zinc carboxypeptidases | PF00246 | 87.75 | 257 | 682 |
| | | | | blastx.14 | (AF017639) carboxypeptidase X2 [Mus musculus] | gi 2921092 gb AAC0 4670.1 | 88% | 2 | 922 |

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|---------|---------|-----|----------------|---|--------------------------|------------|-----------|------------|
| HAIHE43 | 1172244 | 44 | blastx.2 | NEURONAL THREAD PROTEIN AD7C-NTP. | sp O60448 O60448 | 41% | 2538 | 1981 |
| HAIHE43 | 966830 | 672 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 4.22 | 275 | 322 |
| HAJAV28 | 948630 | 45 | HMMER 2.1.1 | PFAM: Actin | PF00022 | 35.9 | 120 | 230 |
| HAPOR59 | 712955 | 46 | blastx.2 | Uncharacterized hypothalamus protein HARP11. | sp AAF67655 AAF67 655 | 97% | 96 | 458 |
| HBIIF78 | 772797 | 673 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 6.42 | 102 | 146 |
| HCDAJ15 | 557243 | 674 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | sp Q9VKB2 Q9VKB 2 | 40% | 3 | 347 |
| HCEIS21 | 671209 | 49 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 3.63 | 60 | 101 |
| HCEJ64 | 951228 | 50 | blastx.2 | hypothetical protein F55G1.5 - Caenorhabditis elegans | PF00099 | 3.61 | 68 | 88 |
| HCEJ64 | 951228 | 50 | HMMER 2.1.1 | PFAM: Peptidase family M13 | PF01431 | 4.17 | 163 | 210 |
| HCEJ64 | 951228 | 50 | blastx.2 | ENDOTHELIN- | sp O60344 ECE2_HU | 60% 43% | 41 224 | 124 292 |
| HCEJ64 | 951228 | 50 | HMMER 2.1.1 | PFAM: Peptidase family M13 | PF01431 | 154.1 | 234 | 563 |
| HCEJ64 | 951228 | 50 | blastx.2 | ENDOTHELIN- | sp O60344 ECE2_HU | 94% | 3 | 599 |

| | | | | CONVERTING ENZYME 2 (EC 3.4.24.71) (ECE-2) 1 | MAN | 59% | 557 | 688 |
|---------|---------|-----|--------------|---|------------------------------|-----------------------------|------------------------------|------------------------------|
| HCFCV92 | 934216 | 675 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 3.55 | 542 | 571 |
| HCFLI54 | 921382 | 52 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 6.41 | 457 | 504 |
| HCFND04 | 1155680 | 53 | blastx.2 | hypothetical protein ZK328.4 - <i>Caenorhabditis elegans</i> | pir T29006 T29006 | 28% | 187 | 1134 |
| HCFND04 | 873441 | 676 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 5.29 | 834 | 881 |
| HCHMV63 | 666798 | 677 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 5.78 | 86 | 133 |
| HCWDL45 | 889416 | 55 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 4.63 | 121 | 168 |
| HCWEI19 | 1125258 | 56 | blastx.2 | alcohol dehydrogenase (EC 1.1.1.1) C - <i>Escherichia coli</i> (isolate VU 3685) | pir S57525 S57525 | 93% | 215 | 436 |
| HCWEI19 | 948690 | 678 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 8.6 | 226 | 273 |
| | | | blastx.14 | formaldehyde dehydrogenase (glutathione) [<i>Escherichia coli</i>] | gi 887431 emb CAA5 2057.1 | 75% | 300 | 10 |
| HCWKB72 | 1224131 | 57 | blastx.2 | SER/ARG-RELATED NUCLEAR MATRIX PROTEIN. | sp O60585 O60585 | .67% .52% 100% 38% | 2613 1482 2049 2637 | 2921 1808 2108 2744 |

| | | | | | | | | |
|---------|---------|-----|--------------------------|---|--------------------------|------------|--------------|--|
| HCWKB72 | 676007 | 679 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 29% | 2613 | 2795 |
| HDDAF49 | 1125713 | 58 | blastx.2 | hypothetical protein DKFZp434D0215.1 - human (fragment) | pir T42650 T42650 | 58% 33% | 912 202 | 2613 2625 2616 2613 2631 2613 2673 2860 2631 |
| HDDAF49 | 911314 | 680 | HMMER 1.8 blastx.2 | PFAM: Zinc-binding metalloprotease domain (AL133047) hypothetical protein [Homo sapiens] | PF00099 | 5.07 | 144 | 173 |
| HDPGQ74 | 691163 | 59 | HMMER 1.8 blastx.2 | PFAM: Zinc-binding metalloprotease domain TTYH1. | emb CAB61374.1 | 52% | 9 | 269 |
| HDPGS68 | 752975 | 60 | HMMER 1.8 blastx.2 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 3.86 | 195 | 236 |
| HDPIX67 | 1172240 | 61 | blastx.2 | ORF2-LIKE PROTEIN (FRAGMENT). | sp AAG02580 AAG0 2580 | 44% | 320 | 3 |
| HDPIX67 | 954385 | 681 | HMMER 2.1.1 | PFAM: Queuine tRNA- ribosyltransferase | sp BAA91131 BAA9 1131 | 65% 60% | 1936 2115 | 2124 2183 |
| | | | | | PF01702 | 40.7 | 86 | 325 |

| | | | | | | | | |
|---------|---------|-----|--------------|--|---|--------------------|-------------------|-------------------|
| | | | blastx.14 | (AE000733) queueine tRNA-ribosyltransferase [Aquifex aeolicus] | gi 2983726 gb AAC0 7288.1 | 35% | 86 | 313 |
| HDPXN01 | 915919 | 682 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF000099 | 4.29 | 99 | 146 |
| HDQFT77 | 1136137 | 63 | blastx.2 | KU70-BINDING PROTEIN (FRAGMENT). | sp Q9Y6H3 Q9Y6H3 | 95% | 98 | 958 |
| HDQFT77 | 932212 | 683 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF000099 | 13.41 | 496 | 534 |
| | | | blastx.14 | (AF078164) Ku70- binding protein [Homo sapiens] | gi 4867999 gb AAD3 1085.1 AF078164_1 | 95% | 13 | 873 |
| HE2FR50 | 508498 | 64 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF000099 | 3.68 | 137 | 166 |
| | | | blastx.2 | hypothetical protein DKFZp547N213.1 - human (fragment) | pir T50613 T50613 | 79% | 122 | 355 |
| HE2SN25 | 948687 | 684 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF000099 | 9.04 | 227 | 268 |
| HE8AE26 | 851514 | 685 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF000099 | 5.8 | 49 | 75 |
| HEBGK01 | 963673 | 67 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF000099 | 4.13 | 426 | 391 |
| | | | blastx.2 | C380A1.2.1 (NOVEL PROTEIN (ISOFORM 1)). | sp Q9UJH9 Q9UJH9 | 81% 85% 100% | 441 743 540 | 112 540 502 |
| HEFMB30 | 691516 | 68 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF000099 | 4.57 | 144 | 185 |
| HEOPE58 | 851009 | 69 | HMMER | PFAM: Zinc-binding | PF000099 | 5.32 | 320 | 364 |

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|---------|---------|-----|-----------------------------------|--|-------------------------------------|-------------------|-------------------|-------------------|
| HETBR74 | 948667 | 70 | 1.8 HMMER 2.1.1 blastx.2 | metalloprotease domain PFAM: Rhodanese-like domain | PF00581 | 32.2 | 321 | 461 |
| | | | | DUAL SPECIFICITY PROTEIN PHOSPHATASE 8 (EC 3.1.3.48) (EC 1 3.1.3.48) | sp O09112 DUS8_M OUSE | 42% 54% 55% | 291 458 535 | 476 523 588 |
| HFCAG94 | 1111177 | 71 | blastx.2 | PRO1722. | sp AAF69605 AAF69 605 | 66% 62% | 860 1008 | 711 850 |
| HFCAG94 | 735763 | 686 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 3.92 | 100 | 129 |
| HFPHR82 | 957528 | 72 | HMMER 2.1.1 blastx.2 | PFAM: Actin Uncharacterized hypothalamus protein HARP11. | PF00022 sp AAF67655 AAF67 655 | 91.7 100% | 1322 1523 | 357 273 |
| HHFO084 | 857780 | 73 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 4.21 | 141 | 161 |
| HISAM68 | 1125189 | 74 | blastx.2 | CDNA FLJ20356 FIS, CLONE HEP15821. | sp BAA91112 BAA9 1112 | 100% | 299 | 75 |
| HISAM68 | 868785 | 687 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 3.48 | 178 | 198 |
| HLHDD45 | 942901 | 75 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 5.88 | 177 | 218 |
| HMMAB49 | 1087684 | 76 | blastx.2 | CDNA FLJ20378 FIS, CLONE KAIA0536. | sp BAA91131 BAA9 1131 | 60% 80% | 678 464 | 466 402 |
| HMMAB49 | 462502 | 688 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 3.49 | 166 | 183 |
| HMSGO27 | 683031 | 77 | blastx.2 | Unnamed portein product. | sp BAB01630 BAB0 1630 | 57% 68% | 77 295 | 238 369 |

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|---------|---------|-----|----------------|---|--------------------------|-------------------|-------------------|-------------------|
| HMSGO27 | 943946 | 689 | HMMER 2.1.1 | PFAM: Reprolysin (M12B) family zinc metalloprotease | PF01421 | 59% | 228 | 293 |
| | | | blastx.2 | (AF137335) metalloprotease disintegrin cysteine-rich protein, secreted form MDC-1s [Homo sapiens] | gb AAD25100.1 | 92% 98% 35% | 232 18 2 | 462 245 103 |
| HNHAM52 | 457010 | 691 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 3.5 | 72 | 89 |
| HNHEQ86 | 785580 | 79 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 3.9 | 7 | 48 |
| HNHFF46 | 859822 | 692 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 5.55 | 3 | 35 |
| HOECV83 | 653276 | 693 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 4.67 | 360 | 389 |
| HORBO54 | 870674 | 82 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 5.64 | 277 | 300 |
| HOSFZ73 | 913876 | 694 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 4.29 | 335 | 355 |
| HPIAU71 | 1123830 | 84 | blastx.2 | ethanolamine ammonia- lyase (EC 4.3.1.7) heavy chain - Escherichia coli (strain K-12) | pir H65018 H65018 | 98% 79% 38% | 400 104 578 | 68 3 516 |
| HPIAU71 | 786811 | 695 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 3.49 | 265 | 291 |
| HRDBT72 | 1112136 | 85 | blastx.2 | PRO1722. | sp AAF69605 AAF69 605 | 73% 75% 57% | 821 673 609 | 666 614 532 |

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|---------|---------|-----|--------------|--|-------------------------------|------------|------------|------------|
| HRDBT72 | 507847 | 696 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 7.31 | 295 | 324 |
| HSDF51 | 1124582 | 86 | blastx.2 | AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) 1 | sp O09175 AMPB_R AT | 33% | 1291 | 872 |
| HSDF51 | 947918 | 697 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 6.14 | 328 | 363 |
| | | | blastx.14 | aminopeptidase-B [Rattus norvegicus] | gi 1754515 dbj BAA1 3413.1 | 31% 36% | 94 289 | 309 420 |
| HSJDM56 | 948669 | 87 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 6.46 | 114 | 149 |
| | | | blastx.2 | formate C- acetyltransferase (EC 2.3.1.54) 1 - Escherichia coli | pir S01788 S01788 | 99% 99% | 811 395 | 395 3 |
| HSICX21 | 531267 | 88 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 3.8 | 307 | 336 |
| HSIDS82 | 531248 | 89 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 5.91 | 206 | 238 |
| HSNAH21 | 571314 | 90 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 7.14 | 91 | 135 |
| HSODC08 | 966264 | 91 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 14.78 | 551 | 510 |
| | | | blastx.2 | BM-014. | sp AAF64270 AAF64 270 | 94% | 779 | 222 |
| HSPAB58 | 736098 | 92 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 4.6 | 39 | 86 |
| HSQCM85 | 963554 | 93 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | 5.37 | 187 | 231 |
| HTOIA82 | 844319 | 94 | HMMER | PFAM: Zinc-binding | PF00099 | 4.25 | 50 | 82 |

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|---------|---------|-----|-----------------------------------|---|--------------------------|-------|------|------|
| HUUDH57 | 931155 | 95 | 1.8 HMMER 2.1.1 blastx.2 | metallopeptidase domain PFAM: Peptidase family M1 | PF01433 | 378.5 | 23 | 661 |
| | | | | ADIPOCYTE-DERIVED LEUCINE AMINOPEPTIDASE. | sp Q9UKY2 Q9UKY 2 | 51% | 2 | 2155 |
| HWACV74 | 1145916 | 96 | blastx.2 | CDNA FLJ20378 FIS, CLONE KAI0536. | sp BAA91131 BAA9 1131 | 52% | 1731 | 1525 |
| HWACV74 | 662347 | 698 | HMMER 1.8 | PFAM: Zinc-binding metallopeptidase domain | PF00099 | 4.43 | 198 | 242 |
| HWAFW39 | 947915 | 97 | HMMER 2.1.1 blastx.2 | PFAM: Peptidase family M1 | PF01433 | 79.5 | 200 | 367 |
| | | | | ADIPOCYTE-DERIVED LEUCINE AMINOPEPTIDASE. | sp Q9UKY2 Q9UKY 2 | 96% | 200 | 367 |
| HWBBR65 | 1156447 | 98 | blastx.2 | NEURONAL THREAD PROTEIN AD7C-NTP. | sp O60448 O60448 | 48% | 1246 | 866 |
| | | | | | | 63% | 1150 | 971 |
| | | | | | | 54% | 703 | 539 |
| | | | | | | 78% | 791 | 708 |
| | | | | | | 50% | 791 | 618 |
| | | | | | | 55% | 1113 | 985 |
| | | | | | | 38% | 840 | 532 |
| | | | | | | 48% | 994 | 803 |
| | | | | | | 62% | 2216 | 2130 |
| | | | | | | 37% | 995 | 753 |
| | | | | | | 60% | 682 | 614 |
| | | | | | | 34% | 703 | 560 |
| | | | | | | 63% | 2241 | 2176 |
| | | | | | | 57% | 767 | 711 |
| | | | | | | 84% | 2215 | 2177 |

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|---------|---------|-----|----------------|--|--------------------------|--|-------|------|------|------|
| | | | | | | | | 32% | 972 | 796 |
| HWBBR65 | 747723 | 699 | HMMER 1.8 | PFAM: Zinc-binding metalloprotease domain | PF00099 | | | 47% | 1129 | 1061 |
| HWMES65 | 969190 | 99 | HMMER 2.1.1 | PFAM: Matrixin | PF00413 | | | 46% | 2183 | 2100 |
| | | | blastx.2 | HATCHING ENZYME PRECURSOR (EC 3.4.24.12) (HE) (HEZ) 1 | sp P91953 HE_HEM PU | | 51% | 606 | 532 | |
| HISBG28 | 920850 | 100 | HMMER 2.1.1 | PFAM: 3'5'-cyclic nucleotide phosphodiesterase | PF00233 | | 195.7 | 625 | 521 | |
| | | | blastx.2 | 3'5'-cyclic-AMP phosphodiesterase (EC 3.1.4.-) - human (fragment) | pir A47286 A47286 | | 90% | 2140 | 2099 | |
| HAAJB60 | 786337 | 101 | HMMER 2.1.1 | PFAM: Aconitase family (aconitate hydratase) | PF00330 | | 72.2 | 185 | 205 | |
| | | | blastx.2 | ACONITATE HYDRATASE, MITOCHONDRIAL PRECURSOR (EC 4.2.1.3) (CITRATE HYDRO-LYASE) (ACONITASE). | sp Q99798 ACON_H UMAN | | 61% | 17 | 109 | |
| HDPDE32 | 1217181 | 102 | blastx.2 | aconitate hydratase (EC | pir G64875 G64875 | | 91% | 69 | 887 | |

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|---------|---------|-----|----------------|---|-------------------------------|--------------------------|-----------------------|-------------------------|
| HDPDE32 | 973342 | 700 | HMMER 2.1.1 | 4.2.1.3) - Escherichia coli PFAM: Aconitase family (aconitate hydratase) | PF00330 | 260.7 | 219 | 569 |
| HBDAC79 | 1199232 | 103 | blastx.2 | ACYL-COENZYME A DEHYDROGENASE-8 PRECURSOR (CDNA FLJ20352 FIS, CLONE HEP14524). | sp Q9UKU7 Q9UKU 7 | 86% 97% 45% | 196 3 452 | 528 203 583 |
| HBDAC79 | 935414 | 701 | HMMER 2.1.1 | PFAM: Acyl-CoA dehydrogenase | PF00441 | 102.6 | 94 | 342 |
| | | | blastx.14 | (AL021958) fadE9 [Mycobacterium tuberculosis] | gi 2911026 emb CAA 17519.1 | 62% 51% 64% 35% | 94 250 348 6 | 255 384 422 89 |
| HEMDX48 | 1163778 | 104 | blastx.2 | ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, 1 | sp P50544 ACDV_M OUSE | 48% | 175 | 1917 |
| HEMDX48 | 521844 | 702 | HMMER 1.8 | PFAM: Acyl-CoA dehydrogenases | PF00441 | 115.91 | 4 | 321 |
| HHASB48 | 721150 | 105 | HMMER 2.1.1 | PFAM: Acyl-CoA dehydrogenase | PF00441 | 101.3 | 319 | 645 |
| | | | blastx.2 | ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, 1 | sp P50544 ACDV_M OUSE | 54% | 175 | 648 |
| HLWCA17 | 1104762 | 106 | blastx.2 | probable acyl-CoA dehydrogenase PA2550 [imported] - Pseudomonas aeruginosa (strain PAO1) | pir D83326 D83326 | 62% | 359 | 979 |

| | | | | | | | | |
|---------|---------|-----|----------------|--|---------------------------|--------------------------|-------------------------|--------------------------|
| HLWCA17 | 957664 | 703 | HMMER 1.8 | PFAM: Acyl-CoA dehydrogenases | PF00441 | 52.61 | 521 | 892 |
| | | | blastx.14 | (AL096811) putative acyl-CoA dehydrogenase [Streptomyces coelicolor A3(2)] | gi 5441764 emb CAB46788.1 | 53% 58% | 521 286 | 904 519 |
| HNTTD09 | 1104487 | 107 | blastx.2 | K09H11.1 PROTEIN. | sp O01590 O01590 | 47% 32% | 179 6 | 832 152 |
| HNTTD09 | 676665 | 704 | HMMER 1.8 | PFAM: Acyl-CoA dehydrogenases | PF00441 | 49.76 | 60 | 425 |
| HSKDT07 | 927823 | 108 | HMMER 1.8 | PFAM: Acyl-CoA dehydrogenases | PF00441 | 122.42 | 13 | 369 |
| | | | blastx.2 | ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, 1 | sp P50544 ACDV_M OUSE | 38% | 7 | 906 |
| HSRDB26 | 1102231 | 109 | blastx.2 | acyl CoA dehydrogenase homolog - Escherichia coli | pir 41124 41124 | 99% 72% 81% | 305 27 2 | 658 305 34 |
| HSRDB26 | 525475 | 705 | HMMER 2.1.1 | PFAM: Acyl-CoA dehydrogenase | PF00441 | 115.7 | 21 | 290 |
| HAPBS07 | 967325 | 110 | HMMER 1.8 | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | 50.05 | 61 | 267 |
| | | | blastx.2 | RETINOL DEHYDROGENASE HOMOLOG. | sp Q9Y2P9 Q9Y2P9 | 75% 69% 62% 34% | 317 61 580 561 | 682 306 708 683 |
| HAUAI17 | 921674 | 111 | HMMER 2.1.1 | PFAM: short chain dehydrogenase | PF00106 | 198.7 | 172 | 687 |

| | | | | | | | | |
|---------|--------|-----|---------------|--|----------------------|-------------------|------------------|-------------------|
| | | | blastx.2 | RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE RETSDR3. | sp Q9UKU3 Q9UKU3 | 81% 100% | 145 687 | 687 857 |
| HBCBT19 | 95953 | 112 | HMME 2.1.1 | PFAM: short chain dehydrogenase | PF00106 | 30.7 | 202 | 417 |
| | | | blastx.2 | hypothetical protein F17A8.100 - Arabidopsis thaliana | pir T04022 T04022 | 40% 41% 52% | 214 38 591 | 552 196 653 |
| HBCPT10 | 957631 | 113 | HMME 1.8 | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | 98.87 | 338 | 673 |
| | | | blastx.2 | CDNA FLJ11008 FIS, CLONE PLACE1003100, MODERATELY SIMILAR 1 | sp BAA91953 BAA91953 | 97% 80% | 263 671 | 670 838 |
| HBGDA14 | 866258 | 114 | HMME 1.8 | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | 127.15 | 3 | 299 |
| | | | blastx.2 | 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase (EC 1.3.1.28) - Escherichia coli | pir A91904 DEECDB | 92% | 3 | 482 |
| HCHNJ32 | 934848 | 115 | HMME 2.1.1 | PFAM: short chain dehydrogenase | PF00106 | 213.6 | 54 | 587 |
| | | | blastx.2 | CARBONYL REDUCTASE | sp Q9UHY9 Q9UHY9 | 95% | 33 | 764 |
| HCHON59 | 931082 | 116 | HMME 2.1.1 | PFAM: SCP-2 sterol transfer family | PF02036 | 96.3 | 1006 | 1335 |

| | | | | | | | | |
|---------|--------|-----|----------------|---|--------------------------|--------|-----|------|
| | | | blastx.2 | CG5590 PROTEIN. | sp Q9VB10 Q9VB10 | 47% | 538 | 1344 |
| HCUGN19 | 716989 | 117 | HMMER 1.8 | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | 68% | 99 | 536 |
| HCUGR38 | 706471 | 118 | HMMER 1.8 | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | 73.02 | 102 | 284 |
| | | | blastx.2 | Putative oxidoreductase. | sp CAB94622 CAB9 4622 | 55% | 105 | 296 |
| HDPND85 | 852628 | 119 | HMMER 1.8 | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | 30% | 4 | 81 |
| | | | blastx.2 | CG9360 PROTEIN. | sp Q9VYU9 Q9VYU 9 | 191.2 | 113 | 709 |
| HDPRN38 | 883658 | 120 | HMMER 1.8 | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | 42% | 113 | 841 |
| | | | blastx.2 | Peroxisomal trans 2-enoyl CoA reductase (EC 1.3.1.8). | sp AAF69798 AAF69 798 | 175.59 | 123 | 680 |
| HE8AM92 | 952610 | 121 | HMMER 1.8 | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | 81% | 111 | 824 |
| | | | blastx.2 | DTDP-4-KETO-6- DEOXY-D-GLUCOSE 4- REDUCTASE. | sp Q9UI54 Q9UI54 | 84% | 61 | 138 |
| HE9RE21 | 888243 | 122 | HMMER 2.1.1 | PFAM: short chain dehydrogenase | PF00106 | 8.98 | 202 | 330 |
| | | | blastx.2 | ESTRADIOL 17 BETA- | sp P56937 DHB7_H | 90% | 208 | 654 |
| | | | | | | 81.3 | 96 | 386 |
| | | | | | | 100% | 90 | 419 |

| | | | | DEHYDROGENASE 7 (EC 1.1.1.62) 1 | UMAN | 88% | 421 | 522 |
|---------|--------|-----|--------------|--|--------------------------|---------------------------|-----------------------|-------------------------|
| HETKH30 | 884009 | 123 | HMMER 1.8 | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | 137.09 | 300 | 881 |
| | | | blastx.2 | PUTATIVE STERIOD DEHYDROGENASE SPM2 (EC 1.1.1.-) | sp O57314 DHBX_A NAPL | 54% | 294 | 866 |
| HHAME78 | 840939 | 124 | HMMER 1.8 | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | 55.01 | 60 | 260 |
| | | | blastx.2 | CARBONYL REDUCTASE. | sp Q9UHY9 Q9UHY 9 | 83% 100% 95% 81% | 48 322 257 2 | 260 426 322 67 |
| HKABI68 | 856590 | 125 | HMMER 1.8 | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | 11.34 | 109 | 285 |
| | | | blastx.2 | HSCARG. | sp AAG09721 AAG0 9721 | 99% 75% | 139 456 | 441 551 |
| HKMLN95 | 914083 | 126 | HMMER 1.8 | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | 100.69 | 23 | 361 |
| | | | blastx.2 | STERIOD DEHYDROGENASE HOMOLOG. | sp Q9Y6G8 Q9Y6G8 | 98% | 20 | 583 |
| HMCFA91 | 959954 | 127 | HMMER 1.8 | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | 25.77 | 19 | 282 |
| | | | blastx.2 | hypothetical protein | pir T04022 T04022 | 53% | 367 | 648 |

| | | | | F17A8.100 - Arabidopsis thaliana | | 41% | 1 | 282 |
|---------|--------|-----|----------------------------|---|----------------------|-------|-----|------|
| HNTBF75 | 836701 | 128 | HMMER 2.1.1 blastx.2 | PFAM: short chain dehydrogenase | PF00106 | 35.2 | 202 | 321 |
| | | | | STEROID DEHYDROGENASE HOMOLOG. | sp Q9Y6G8 Q9Y6G8 | 78% | 52 | 414 |
| HPTGB43 | 726460 | 129 | HMMER 2.1.1 blastx.2 | PFAM: short chain dehydrogenase | PF00106 | 45.1 | 84 | 191 |
| | | | | CARBONYL REDUCTASE. | sp Q9UHY9 Q9UHY 9 | 73% | 87 | 374 |
| HPTVL90 | 509487 | 130 | HMMER 2.1.1 blastx.2 | PFAM: short chain dehydrogenase | PF00106 | 46.3 | 11 | 115 |
| HSKIA89 | 837986 | 131 | | RETINAL SHORT- CHAIN DEHYDROGENASE/RE DUCTASE RETSDR3. | sp Q9UKU3 Q9UKU 3 | 76% | 8 | 319 |
| | | | HMMER 1.8 blastx.2 | PFAM: Alcohol/other dehydrogenases, short chain type | PF00106 | 17.7 | 359 | 478 |
| HTXGF27 | 695766 | 132 | | hypothetical protein T11F9.11 - Caenorhabditis elegans | pir T24832 T24832 | 42% | 329 | 619 |
| | | | HMMER 2.1.1 blastx.2 | PFAM: short chain dehydrogenase | PF00106 | 53% | 123 | 320 |
| HWHHW54 | 684125 | 133 | | hypothetical protein DKFZp566O084.1 - human | pir T17307 T17307 | 35% | 737 | 820 |
| | | | HMMER 2.1.1 | PFAM: short chain dehydrogenase | PF00106 | 208.7 | 193 | 765 |
| | | | | | | 93% | 70 | 1011 |
| | | | | | | 100% | 38 | 73 |
| | | | | | | 59.1 | 871 | 1002 |

| | | | blastx.2 | Oxidoreductase UCPA. | sp AAF80754 AAF80754. | 77% | 871 | 1059 |
|----------|---------|-----|-------------------------|---|---------------------------------|---------------------|------------------|-------------------|
| HWHPO29 | 857383 | 134 | HMMER 2.1.1 blastx.2 | PFAM: short chain dehydrogenase CGI-82 PROTEIN. | PF00106 | 101.3 | 257 | 664 |
| HWLPR94 | 967326 | 135 | HMMER 1.8 | PFAM: Alcohol/other dehydrogenases, short chain type | sp Q9Y391 Q9Y391 | 74% 64% | 257 186 | 664 260 |
| | | | blastx.2 | RETINOL DEHYDROGENASE HOMOLOG. | PF00106 | 44.2 | 193 | 417 |
| HWLJUL28 | 925331 | 136 | HMMER 1.8 blastx.2 | PFAM: Alcohol/other dehydrogenases, short chain type C359F1.1 (novel protein (ortholog of mouse and rat 1 | sp Q9Y2P9 Q9Y2P9 | 95% 84% | 184 36 | 450 134 |
| | | | | | PF00106 | 113.24 | 163 | 588 |
| | | | | | sp CAB92744 CAB92744 | 82% | 97 | 735 |
| HWLXT48 | 957630 | 137 | HMMER 1.8 blastx.2 | PFAM: Alcohol/other dehydrogenases, short chain type CDNA FLJ11008 FIS, CLONE PLACE1003100, MODERATELY SIMILAR 1 | PF00106 sp BAA91953 BAA91953 | 46.57 83% 94% | 133 58 309 | 306 333 359 |
| HGMD15 | 1103922 | 138 | blastx.2 | L-threonine 3-dehydrogenase (EC 1.1.1.103) - Escherichia coli | pit A33276 DEECTH | 91% 79% | 64 554 | 564 655 |
| HGMD15 | 786307 | 706 | HMMER | PFAM: Zinc-binding | PF00107 | 141.1 | 3 | 323 |

| | | | | | | | | |
|---------|---------|-----|-----------------------------------|--|------------------------------|----------------------------|--------------------------|--------------------------|
| HNGMA91 | 789744 | 139 | 2.1.1 HMMER 1.8 blastx.2 | dehydrogenases PFAM: Zinc-binding dehydrogenases probable alcohol dehydrogenase (EC 1.1.1.1) ybdR - Escherichia coli | PF00107 pir F64794 F64794 | 28.74 92% | 76 76 | 231 318 |
| HSLEI57 | 1103672 | 140 | blastx.2 | alcohol dehydrogenase (EC 1.1.1.1) C - Escherichia coli | pir D64763 D64763 | 87% | 74 | 565 |
| HSLEI57 | 730927 | 707 | HMMER 2.1.1 blastx.2 | PFAM: Zinc-binding dehydrogenases probable oxidoreductase (EC 1.1.1.-) ycjQ - Escherichia coli | PF00107 pir D64880 D64880 | 236 95% | 5 2 | 388 994 |
| HSLFE21 | 823083 | 708 | HMMER 1.8 blastx.2 | PFAM: Zinc-binding dehydrogenases probable alcohol dehydrogenase (EC 1.1.1.1) ybdR - Escherichia coli | PF00107 pir F64794 F64794 | 76.21 97% | 344 88 | 655 510 |
| HSLIE40 | 866274 | 709 | HMMER 1.8 blastx.2 | PFAM: Zinc-binding dehydrogenases CGI-63 PROTEIN. | PF00107 sp Q9Y373 Q9Y373 | 30.97 98% 72% | 152 309 14 | 283 836 190 |
| HTXHA35 | 1152110 | 143 | HMMER 1.8 blastx.2 | PFAM: Zinc-binding dehydrogenases ALDO-KETO REDUCTASE. | PF00107 sp O09125 O09125 | 53.56 75% 75% 63% | 265 193 535 733 | 471 480 738 798 |

| | | | | | | | | |
|---------|---------|-----|-----------------------------|--|---|---|---------------------------------------|---|
| HAICS07 | 953351 | 711 | HMMER 2.1.1 blastx.14 | PFAM: Aldo/keto reductase family aldo-keto reductase [Mus musculus] | PF00248 | 283 | 193 | 480 |
| HBKDN33 | 1167313 | 145 | blastx.2 | Acetyl-CoA synthetase. | sp AAF75064 AAF75 064 | 85% 85% | 2 955 | 1015 1014 |
| HBKDN33 | 922414 | 712 | HMMER 2.1.1 blastx.14 | PFAM: AMP-binding enzyme acetyl-CoA synthetase [Drosophila melanogaster] | PF00501 | 249.5 | 2 | 931 |
| HBODH62 | 1228278 | 146 | blastx.2 | DJ568C11.3 (novel AMP- binding enzyme similar to 1 | gi 608694 emb CAA8 6738.1 sp CAB75500 CAB7 5500 | 65% 98% 100% | 2 344 297 | 1222 1696 362 |
| HBODH62 | 742827 | 713 | HMMER 1.8 blastx.2 | PFAM: AMP-binding enzymes | PF00501 | 43.02 | 27 | 158 |
| HCEPJ44 | 1157810 | 147 | blastx.2 | Sequence 17 from Patent WO951740. | sp CAC07591 CAC0 7591 | 99% | 2 | 571 |
| HCEPJ44 | 930790 | 714 | HMMER 1.8 blastx.14 | PFAM: AMP-binding enzymes (AF023258) fatty acid transport protein [Mus musculus] | PF00501 | 19.17 | 3 | 215 |
| HCWCM65 | 1105668 | 148 | blastx.2 | probable non-ribosomal peptide synthetase PA2402 [imported] - Pseudomonas aeruginosa (strain PAO1) | gi 2612939 gb AAC6 9640.1 pir F83345 F83345 | 90% 75% 74% 37% 31% 57% 53% | 9 12 12 9 9 595 595 | 536 611 611 605 596 678 678 |
| HCWCM65 | 529230 | 715 | HMMER | PFAM: AMP-binding | PF00501 | 69.62 | 31 | 264 |

| | | | | | | | | |
|---------|---------|-----|---------------------------|--|--|---|---------------------------------------|---|
| HDQDY52 | 1182322 | 149 | 1.8 blastx.2 | enzymes DJ18C9.1 (SIMILAR TO ACETYL-COENZYME A SYNTHETASE) 1 | sp Q9UJ15 Q9UJ15 | 84% 81% 55% | 85 566 705 | 690 778 785 |
| HDQDY52 | 852622 | 716 | HMMER 1.8 blastx.2 | PFAM: AMP-binding enzymes (AL049709) dJ18C9.1 (similar to acetyl- coenzyme A synthetase) [Homo sapiens] | PF00501 emb CAB61786.1 | 82.8 84% 81% 55% | 316 85 566 705 | 555 690 778 785 |
| HEEAA32 | 1203140 | 150 | blastx.2 | CDNA FLJ20581 FIS, CLONE REC00491. | sp BAA91273 BAA9 1273 | 93% 97% 57% | 502 3 1146 | 1182 500 1208 |
| HEEAA32 | 887490 | 717 | HMMER 1.8 | PFAM: AMP-binding enzymes | PF00501 | 35.92 | 39 | 407 |
| HEGAN70 | 839719 | 151 | HMMER 1.8 blastx.2 | PFAM: AMP-binding enzymes Hypothetical 179.7 kDa protein. | PF00501 sp AAF64300 AAF64 300 | 18.6 61% 85% 34% 54% | 334 124 31 295 748 | 516 654 111 579 846 |
| HFKMF42 | 1104119 | 152 | blastx.2 | Long-chain-fatty-acid- CoA ligase-like protein. | sp BAB02683 BAB0 2683 | 48% 41% | 656 65 | 1096 556 |
| HFKMF42 | 923824 | 718 | HMMER 1.8 blastx.14 | PFAM: AMP-binding enzymes 4-coumarate-coA ligase [Mycobacterium leprae] | PF00501 gi 699196 gb AAA62 961.1 | 91.1 51% 48% 55% 36% 50% | 86 764 647 365 968 491 | 901 949 781 484 1099 568 |

| | | | | | | | | |
|---------|---------|-----|-----------------------------|---|---|----------------------|-----------|-------------------|
| HFPHG06 | 1104964 | 153 | blastx.2 | enterobactin synthetase component F - Escherichia coli | pir H64791 YGECEF | 53% 44% | 65 570 | 103 623 |
| HFPHG06 | 933802 | 719 | HMMER 2.1.1 blastx.14 | PFAM: AMP-binding enzyme enterobactin [Escherichia coli] | PF00501 gi 145843 gb AAA92 015.1 | 66 90% | 53 2 | 232 220 |
| HHEMB89 | 1227613 | 154 | blastx.2 | DJ568C11.3 (novel AMP- binding enzyme similar to 1 | sp CAB75500 CAB7 5500 | 99% | 561 | 1961 |
| HHEMB89 | 574897 | 720 | HMMER 2.1.1 | PFAM: AMP-binding enzyme | PF00501 | 115.4 | 1 | 453 |
| HLDPC46 | 466567 | 155 | HMMER 1.8 blastx.2 | PFAM: AMP-binding enzymes CDNA FLJ20581 FIS, CLONE REC00491. | PF00501 sp BAA91273 BAA9 1273 | 103.84 89% 57% | 17 586 | 481 571 681 |
| HLDRG44 | 1106225 | 156 | blastx.2 | KIDNEY-SPECIFIC PROTEIN. | sp O70490 O70490 | 74% | 16 | 1011 |
| HLDRG44 | 969544 | 721 | HMMER 1.8 blastx.14 | PFAM: AMP-binding enzymes (AF062389) kidney- specific protein [Rattus norvegicus] | PF00501 gi 3127193 gb AAD0 5209.1 | 104.64 78% | 89 2 | 694 931 |
| HLICR73 | 1107517 | 157 | blastx.2 | VERY LONG-CHAIN ACYL-COA SYNTHETASE HOMOLOG 2. | sp Q9Y2P5 Q9Y2P5 | 96% | 9 | 536 |
| HLICR73 | 837030 | 722 | HMMER | PFAM: AMP-binding | PF00501 | 20.33 | 19 | 324 |

| | | | | | | | | |
|---------|---------|-----|-----------------------------|---|-------------------------------------|-------------|------------|------------|
| | | | 1.8 blastx.2 | enzymes (AF064255) very long-chain acyl-CoA synthetase homolog 2; VLCS-H2 [Homo sapiens] | gb AAD29444.1 AF064255_1 | 99% 100% | 1 450 | 441 497 |
| HNHOP64 | 1103943 | 158 | blastx.2 | FATTY ACID TRANSPORT PROTEIN. PFAM: AMP-binding enzymes | sp O95186 O95186 | 90% 52% | 515 57 | 57 1 |
| HNHOP64 | 966754 | 723 | HMMER 1.8 blastx.14 | (AF055899) fatty acid transport protein [Homo sapiens] | PF00501 | 23.65 | 539 | 757 |
| HSDEF56 | 1128288 | 159 | blastx.2 | acetate--CoA ligase (EC 6.2.1.1) - Escherichia coli | gi 4206376 gb AAD11623.1 | 88% 52% | 374 835 | 835 891 |
| HSDEF56 | 496551 | 724 | HMMER 2.1.1 | PFAM: AMP-binding enzyme | PF00501 | 175.3 | 2 | 436 |
| HTENI29 | 1105518 | 160 | blastx.2 | LONG-CHAIN ACYL-COA SYNTHETASE 5. | sp Q9UKU0 Q9UKU0 | 97% | 24 | 1172 |
| HTENI29 | 954519 | 725 | HMMER 1.8 blastx.14 | PFAM: AMP-binding enzymes (AF129166) long-chain acyl-CoA synthetase 5 [Homo sapiens] | PF00501 | 65 | 366 | 845 |
| HWMKD72 | 1106729 | 161 | blastx.2 | agmatinase PA1421 [imported] - Pseudomonas aeruginosa (strain PAO1) | gi 5702202 gb AAD47199.1 AF129166_1 | 98% | 51 | 1172 |
| HWMKD72 | 970613 | 726 | HMMER 2.1.1 blastx.14 | PFAM: Arginase family agmatine ureohydrolase | PF00491 | 179.6 | 11 | 565 |
| | | | | | gi 882466 gb AAA69 | 48% | 302 | 625 |

| | | | | | | | | | | |
|---------|---------|-----|----------------------------|--|--|--------------------------|--|-------------|-----------|--------------|
| | | | | | [Escherichia coli] | 104.1 | | 50% | 14 | 166 |
| HAPSQ21 | 972037 | 162 | HMMER 2.1.1 | | PFAM: Eukaryotic aspartyl protease | PF00026 | | 44% | 164 | 271 |
| | | | blastx.2 | | NAPSIN 1 PRECURSOR (EC 3.4.23.-) (NAPSIN A) (NAPA) 1 | sp O96009 NAP1_H UMAN | | 274.4 | 211 | 735 |
| HLJDW02 | 1192885 | 163 | blastx.2 | | NAPSIN 1 PRECURSOR (EC 3.4.23.-) (NAPSIN A) (NAPA) 1 | sp O96009 NAP1_H UMAN | | 100% 90% | 58 767 | 762 865 |
| HLJDW02 | 837592 | 727 | HMMER 2.1.1 blastx.2 | | PFAM: Eukaryotic aspartyl protease (AF090386) napsin A [Homo sapiens] | PF00026 | | 134.5 | 65 | 412 |
| HMGBT01 | 1205666 | 164 | blastx.2 | | aspartic proteinase (EC 3.4.23.-) BACE precursor - human | gb AAD04917.1 | | 100% 65% | 47 433 | 433 534 |
| HMGBT01 | 879904 | 728 | HMMER 1.8 | | PFAM: Eukaryotic aspartyl proteases | PF00026 | | 31.46 | 3 | 362 |
| HSSJJ24 | 1178041 | 165 | blastx.2 | | aspartic proteinase (EC 3.4.23.-) BACE precursor - human | pir A59090 A59090 | | 100% 85% | 8 1714 | 1081 2001 |
| HSSJJ24 | 905092 | 729 | HMMER 1.8 | | PFAM: Eukaryotic aspartyl proteases | PF00026 | | 26.48 | 33 | 113 |
| HFTCG46 | 669383 | 166 | HMMER 2.1.1 blastx.2 | | PFAM: Eukaryotic-type carbonic anhydrase | PF00194 | | 101.7 | 78 | 266 |
| | | | | | CARBONIC ANHYDRASE VB, MITOCHONDRIAL PRECURSOR (EC 1 | sp Q9Y2D0 CA5B_H UMAN | | 98% | 78 | 257 |

| | | | | | | | | |
|---------|---------|-----|----------------|--|--------------------------|-------------------|------------------|-------------------|
| HNTMD81 | 929511 | 167 | HMMER 2.1.1 | PFAM: Bukaryotic-type carbonic anhydrase | PF00194 | 84.3 | 16 | 249 |
| | | | blastx.2 | CARBONIC ANHYDRASE XIV PRECURSOR (EC 4.2.1.1) (CARBONATE 1 | sp Q9ULX7 CAHE_ HUMAN | 69% 69% 90% | 19 135 434 | 369 437 499 |
| HBSAJ60 | 1174334 | 168 | blastx.2 | OUTER MEMBRANE USHER PROTEIN PMFC PRECURSOR. | sp Q9R7S7 Q9R7S7 | 99% 97% | 2043 2888 | 2885 3331 |
| HBSAJ60 | 573965 | 730 | HMMER 2.1.1 | PFAM: Citrate synthase | PF00285 | 192 | 2 | 265 |
| HSKCI43 | 506599 | 169 | HMMER 1.8 | PFAM: Citrate synthase | PF00285 | 69.36 | 1 | 315 |
| | | | blastx.2 | citrate (si)-synthase (EC 4.1.3.7) - Escherichia coli | pir G64807 YKEC | 64% 96% | 1 168 | 345 260 |
| HSDKE47 | 1128095 | 170 | blastx.2 | NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NDUFS2 precursor - human | pir JE0193 JE0193 | 100% | 73 | 195 |
| HSDKE47 | 764970 | 731 | HMMER 2.1.1 | PFAM: Respiratory-chain NADH dehydrogenase, 49 Kd subunit | PF00346 | 79.8 | 64 | 195 |
| HCWTB56 | 1172460 | 171 | blastx.2 | probable cation- transporting P-type ATPase PA2435 [imported] - Pseudomonas aeruginosa (strain PAO1) | pir F83342 F83342 | 65% 95% | 2 270 | 268 332 |
| HCWTB56 | 853009 | 732 | HMMER 1.8 | PFAM: E1-E2 ATPases | PF00122 | 55.15 | 2 | 301 |
| | | | blastx.2 | cadmium resistance | gb AAB37345.1 | 42% | 2 | 316 |

| | | | | | | | | |
|---------|---------|-----|----------------|---|--------------------------|-------------------|------------------|-------------------|
| HFPBS73 | 1144027 | 172 | blastx.2 | protein [Lactococcus lactis] H+/K+-exchanging ATPase (EC 3.6.1.36) chain B [validated] - Escherichia coli | pir H64804 PWECB K | 81% | 373 | 1122 |
| HFPBS73 | 954892 | 733 | HMMER 2.1.1 | PFAM: E1-E2 ATPase | PF00122 | 196.5 | 3 | 572 |
| | | | blastx.2 | kdpB [Escherichia coli] | gb AAB96336.1 | 100% 100% | 3 580 | 563 603 |
| HOEDD44 | 954893 | 173 | HMMER 2.1.1 | PFAM: E1-E2 ATPase | PF00122 | 173.2 | 53 | 574 |
| | | | blastx.2 | H+/K+-exchanging ATPase (EC 3.6.1.36) chain B [validated] - Escherichia coli | pir H64804 PWECB K | 92% 96% 39% | 53 634 513 | 574 723 635 |
| HSUAN33 | 956315 | 174 | HMMER 1.8 | PFAM: E1-E2 ATPases | PF00122 | 46.29 | 1317 | 907 |
| | | | blastx.2 | Hypothetical 128.8 kDa protein. | sp CAB89728 CAB8 9728 | 48% 35% | 1596 693 | 766 256 |
| HBCMD49 | 1206021 | 175 | blastx.2 | hypothetical protein F38H4.8 - Caenorhabditis elegans | pir T21981 T21981 | 44% | 46 | 357 |
| HBCMD49 | 865314 | 734 | HMMER 2.1.1 | PFAM: Enoyl-CoA hydratase/isomerase family | PF00378 | 74.6 | 263 | 550 |
| | | | blastx.2 | (AE000989) enoyl-CoA hydratase (fad-4) [Archaeoglobus fulgidus] | gb AAB89601.1 | 39% | 197 | 619 |
| HKABN12 | 956826 | 176 | HMMER | PFAM: Enoyl-CoA | PF00378 | 31.8 | 900 | 820 |

| | | | | | | | | | | |
|---------|---------|-----|-------------|--|---------------------------|-------|------|------|--|--|
| | | | 2.1.1 | hydratase/isomerase family | | | | | | |
| | | | blastx.2 | CG6984 PROTEIN. | sp Q9V7Y3 Q9V7Y3 | 37% | 745 | 593 | | |
| | | | | | | 41% | 891 | 739 | | |
| HMOAC31 | 1228291 | 177 | blastx.2 | probable 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) ydbU - Escherichia coli (strain K-12) | pir F64890 F64890 | 93% | 1297 | 2586 | | |
| HMOAC31 | 920386 | 735 | HMMER 2.1.1 | PFAM: Enoyl-CoA hydratase/isomerase family | PF00378 | 159.1 | 5 | 268 | | |
| | | | blastx.14 | enoyl-CoA hydratase [Escherichia coli] | gi 2764828 emb CAA66095.1 | 88% | 2 | 355 | | |
| | | | | | | 90% | 334 | 495 | | |
| HMVBO92 | 1204710 | 178 | blastx.2 | CDNA FLJ10948 FIS, CLONE PLACE1000142, WEAKLY SIMILAR TO 1 | sp BAA91922 BAA91922 | 99% | 1701 | 2090 | | |
| HMVBO92 | 791284 | 736 | HMMER 1.8 | PFAM: Enoyl-CoA hydratase/isomerase | PF00378 | 32.87 | 167 | 274 | | |
| HOELA62 | 1228151 | 179 | blastx.2 | CDNA FLJ10948 FIS, CLONE PLACE1000142, WEAKLY SIMILAR TO 1 | sp BAA91922 BAA91922 | 98% | 1685 | 2074 | | |
| HOELA62 | 863712 | 737 | HMMER 2.1.1 | PFAM: Enoyl-CoA hydratase/isomerase family | PF00378 | 39.5 | 1635 | 1757 | | |
| HSSGE35 | 1228152 | 180 | blastx.2 | CDNA FLJ10948 FIS, CLONE PLACE1000142, | sp BAA91922 BAA91922 | 89% | 97 | 498 | | |

| | | | | | WEAKLY SIMILAR TO 1 | | | | | |
|---------|---------|-----|----------------|-----------|---|-------------------------------|-------------------|-------------------|--------------------|--|
| HSSGE35 | 967832 | 738 | HMMER 1.8 | blastx.14 | PFAM: Enoyl-CoA hydratase/isomerase | PF00378 | 39.59 | 70 | 210 | |
| | | | | | AU-binding protein/Enoyl-CoA hydratase [Homo sapiens] | gi 780241 emb CAA5 6260.1 | 57% 55% 69% | 88 1 363 | 357 87 401 | |
| HEMF174 | 1216651 | 181 | blastx.2 | | GLUCOSAMINE-- FRUCTOSE-6- PHOSPHATE AMINOTRANSFERASE 11 | sp O94808 GFA2_H UMAN | 100% 98% | 193 1301 | 1299 1468 | |
| HEMF174 | 523350 | 739 | HMMER 2.1.1 | | PFAM: Glutamine amidotransferases class-II | PF00310 | 74.1 | 124 | 348 | |
| HISCL24 | 676997 | 182 | HMMER 2.1.1 | | PFAM: Glutamine amidotransferases class-II | PF00310 | 92.7 | 3 | 233 | |
| | | | blastx.2 | | GLUCOSAMINE-- FRUCTOSE-6- PHOSPHATE AMINOTRANSFERASE 11 | sp O94808 GFA2_H UMAN | 85% | 3 | 560 | |
| H7PBB83 | 1228150 | 183 | blastx.2 | | CG9630 PROTEIN. | sp Q9VHU1 Q9VHU 1 | 47% 56% 25% | 145 955 776 | 774 1044 871 | |
| H7PBB83 | 908235 | 740 | HMMER 1.8 | | PFAM: Helicases conserved C-terminal domain | PF00271 | 84.64 | 756 | 586 | |
| | | | blastx.14 | | (AJ010469) RNA helicase [Arabidopsis thaliana] | gi 3776011 emb CAA 09208.1 | 54% 49% | 756 516 | 514 310 | |
| HAGBA63 | 1122199 | 184 | blastx.2 | | PUTATIVE ATP- | sp O43630 O43630 | 99% | 1121 | 78 | |

| | | | | DEPENDENT MITOCHONDRIAL RNA HELICASE. | | | | | |
|---------|---------|-----|---------------------------|--|---|--|---|---|--|
| HAGBA63 | 509775 | 741 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 7.62 | 2 | 124 | |
| HBMUG47 | 1102698 | 185 | blastx.2 | RECQ HELICASE 5 (DNA HELICASE RECQ5 GAMMA). | sp Q9UNC8 Q9UNC 8 | 98% | 21 | 530 | |
| HBMUG47 | 863846 | 742 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 52.06 | 22 | 204 | |
| HCRPZ84 | 1130816 | 186 | blastx.2 | RNA helicase. | sp AAG09428 AAG0 9428 | 37% 25% 34% 40% | 3 1469 1161 834 | 893 1942 1640 1013 | |
| HCRPZ84 | 963476 | 743 | HMMER 1.8 blastx.14 | PFAM: Helicases conserved C-terminal domain (AF038963) RNA helicase [Homo sapiens] | PF00271 gi 4405795 gb AAD1 9826.1 | 13.09 | 923 | 1063 | |
| | | | | | | 45% 43% 59% 50% 56% 45% 30% 44% | 137 506 26 1063 413 863 737 1154 | 373 622 91 1140 460 934 853 1228 | |
| HCWTR54 | 1192287 | 187 | blastx.2 | NEURONAL THREAD PROTEIN AD7C-NTP. | sp O60448 O60448 | 64% 69% 48% | 304 245 313 | 179 120 233 | |

| | | | | | | | | |
|---------|---------|-----|----------------|--|------------------------------|-------|------|------|
| HCWTR54 | 729290 | 744 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 27% | 331 | 233 |
| HDPBB41 | 1195686 | 188 | blastx.2 | RNA helicase HEL117 - rat | pir A57514 A57514 | 85% | 364 | 344 |
| HDPBB41 | 925800 | 745 | HMMER 2.1.1 | PFAM: Helicases conserved C-terminal domain | PF00271 | 6.14 | 151 | 198 |
| HEOPI32 | 907903 | 189 | blastx.14 | (AF106680) RNA helicase [Homo sapiens] | gi 5410326 gb AAD4 3033.1 | 90% | 2411 | 564 |
| HFSAG03 | 1151479 | 190 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 88% | 2722 | 2372 |
| HFSAG03 | 960973 | 746 | blastx.2 | DJ620E11.1A (NOVEL HELICASE C- TERMINAL DOMAIN AND SNF2 1 1 | sp Q9UJF0 Q9UJF0 | 45% | 2814 | 2545 |
| HFXCI24 | 1182719 | 191 | blastx.2 | probable ATP-dependent RNA helicase rhIE - Escherichia coli | pir E64816 E64816 | 108.7 | 47 | 292 |
| HFXCI24 | 908374 | 747 | HMMER 2.1.1 | PFAM: Helicases conserved C-terminal domain | PF00271 | 82% | 17 | 637 |
| HFSAG03 | 1151479 | 190 | blastx.2 | PRO0478. | sp Q9UJ59 Q9UJ59 | 89.44 | 176 | 430 |
| HFSAG03 | 960973 | 746 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 87% | 2 | 661 |
| HFXCI24 | 1182719 | 191 | blastx.2 | probable ATP-dependent RNA helicase rhIE - Escherichia coli | pir E64816 E64816 | 67% | 967 | 1086 |
| HFXCI24 | 908374 | 747 | HMMER 2.1.1 | PFAM: Helicases conserved C-terminal domain | PF00271 | 6.39 | 454 | 365 |
| HFXCI24 | 908374 | 747 | HMMER 2.1.1 | PFAM: Helicases conserved C-terminal domain | PF00271 | 81% | 12 | 674 |
| HFXCI24 | 908374 | 747 | HMMER 2.1.1 | PFAM: Helicases conserved C-terminal domain | PF00271 | 128.5 | 151 | 396 |

| | | | | | | | | | |
|---------|---------|-----|--|--------------|--|---------------------------|-------------------|------------------|--------------------|
| | | | | blastx.14 | Putative ATP-dependent RNA helicase RhlE. [Escherichia coli] | gi 4062355 dbj BAA35457.1 | 94% 100% | 1 644 | 543 664 |
| HFXHJ89 | 907938 | 192 | | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 88.81 | 216 | 470 |
| | | | | blastx.2 | DJ620E11.1A (NOVEL HELICASE C-TERMINAL DOMAIN AND SNF2 1 1 | sp Q9UJF0 Q9UJF0 | 98% 78% 48% | 210 37 5 | 881 207 85 |
| HHPTC55 | 1106390 | 193 | | blastx.2 | hypothetical protein C27B7.4 - Caenorhabditis elegans | pir T19508 T19508 | 47% | 2 | 541 |
| HHPTC55 | 907951 | 748 | | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 61.91 | 13 | 243 |
| | | | | blastx.14 | (AF026032) ATRX protein [Mus musculus] | gi 3002558 gb AAC08741.1 | 54% | 4 | 351 |
| HJB54 | 1195070 | 194 | | blastx.2 | DJ616B8.1 (RNA HELICASE) (Fragment). | sp CAC03449 CAC03449 | 89% | 3 | 551 |
| HJB54 | 869621 | 749 | | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 10.61 | 3 | 170 |
| | | | | blastx.2 | (AC005314) putative pre-mRNA splicing factor RNA helicase [Arabidopsis thaliana] | gb AAC36188.1 | 54% | 3 | 563 |
| HKAHB56 | 1162649 | 195 | | blastx.2 | RNA helicase. | sp AAG09428 AAG09428 | 28% 31% 33% | 833 333 54 | 1606 824 389 |

| | | | | | | | | |
|---------|---------|-----|--------------|---|-------------------------------|-------------------|-----------------|--------------------|
| HKAHB56 | 865298 | 750 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 63.37 | 699 | 986 |
| HLDCI35 | 1151490 | 196 | blastx.2 | APOBEC-1 stimulating protein. | sp CAB94754 CAB9 4754 | 83% | 84 | 725 |
| HLDCI35 | 831356 | 751 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 6.01 | 288 | 374 |
| | | | blastx.2 | (AF209192) Apobec-1 complementation factor [Homo 1 | gb AAF34824.1 AF2 09192_1 | 94% | 177 | 725 |
| HMCBU79 | 1165318 | 197 | blastx.2 | CDNA FLJ20110 FIS, CLONE COL05103. | sp BAA90955 BAA9 0955 | 89% | 1 | 987 |
| HMCBU79 | 856630 | 752 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 17.95 | 349 | 459 |
| HNTRV07 | 1199546 | 198 | blastx.2 | Cytoplasmic dynein heavy chain. | sp BAA97048 BAA9 7048 | 92% 91% 40% | 934 18 48 | 2001 923 152 |
| HNTRV07 | 952794 | 753 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 6.41 | 274 | 345 |
| | | | blastx.14 | similar to dynein heavy chain; cDNA EST EMBL:D27549.1 [Caenorhabditis elegans] | gi 3876099 emb CAA 99830.1 | 33% | 46 | 333 |
| HODEX10 | 926260 | 754 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 9.2 | 22 | 54 |
| HOGAQ10 | 1222600 | 200 | blastx.2 | Proliferation-associated | sp AAF82262 AAF82 | 99% | 1045 | 1992 |

| | | | | | | | | |
|---------|---------|-----|--------------|--|-----------------------------|------------|--------------|--------------|
| HOGAQ10 | 907911 | 755 | HMMER 1.8 | SNF2-like protein. PFAM: Helicases conserved C-terminal domain | 262 | 94% | 98 | 1051 |
| | | | blastx.14 | lymphocyte specific helicase [Mus musculus] | gi 805296 gb AAB08 015.1 | 93% 83% | 80 18 | 556 71 |
| HOSBW20 | 985056 | 201 | blastx.2 | CG7972 PROTEIN. | sp Q9VSE2 Q9VSE2 | 47% | 4 | 777 |
| HOSBW20 | 668774 | 756 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 13.94 | 58 | 96 |
| HRADL60 | 1151310 | 202 | blastx.2 | probable pre-mRNA splicing factor ATP- dependent RNA helicase - fission yeast (Schizosaccharomyces pombe) | pir T37496 T37496 | 40% 42% | 2750 2750 | 1416 1737 |
| HRADL60 | 967578 | 757 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 14.84 | 248 | 496 |
| | | | blastx.2 | (AL009197) putative pre- mRNA splicing factor ATP-dependent RNA helicase [Schizosaccharomyces pombe] | emb CAA15715.1 | 40% 44% | 83 83 | 1429 1096 |
| HSGSC29 | 1150837 | 203 | blastx.2 | ACTIN INTERACTING PROTEIN. | sp O23240 O23240 | 56% | 334 | 750 |
| HSGSC29 | 953599 | 758 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 9.31 | 345 | 446 |

| | | | | | | | | |
|---------|---------|-----|--------------|---|---|-------------------|-----------------|--------------------|
| | | | blastx.14 | actin interacting protein [Arabidopsis thaliana] | gi 4006920 emb CAB 16815.1 | 53% | 468 | 740 |
| HTEDX38 | 1106208 | 204 | blastx.2 | DEAD-BOX PROTEIN. | sp Q9Y6S9 Q9Y6S9 | 70% | 333 | 452 |
| HTEDX38 | 920697 | 759 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 90% | 55 | 1494 |
| | | | blastx.14 | (AF106019) DEAD-box protein [Homo sapiens] | gi 5359631 gb AAD4 2744.1 AF106019_1 | 90% | 3 | 176 |
| HTEJE15 | 1102531 | 205 | blastx.2 | VASA protein. | sp AAF72705 AAF72 705 | 100% | 1 | 405 |
| HTEJE15 | 908360 | 760 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 14.92 | 5 | 52 |
| | | | blastx.14 | vasa-like gene protein, RVLG protein=putative DEAD 1 [Rattus sp.] | gi 806464 gb AAB33 364.1 | 73% 84% 65% | 2 242 188 | 190 319 265 |
| HTOES03 | 1150877 | 206 | blastx.2 | TRANSCRIPTIONAL ACTIVATOR SRCAP. | sp Q9Y5L9 Q9Y5L9 | 40% | 203 | 1186 |
| HTOES03 | 955814 | 761 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 53.97 | 240 | 491 |
| | | | blastx.14 | (AF143946) transcriptional activator SRCAP [Homo sapiens] | gi 5106572 gb AAD3 9760.1 AF143946_1 | 50% 39% 33% | 6 906 540 | 569 1019 656 |
| HTOHS18 | 1193057 | 207 | blastx.2 | ATP-DEPENDENT RNA HELICASE. | sp Q9SHB9 Q9SHB9 | 39% | 39 | 857 |
| HTOHS18 | 908347 | 762 | HMMER 1.8 | PFAM: Helicases conserved C-terminal domain | PF00271 | 104.65 | 158 | 370 |
| | | | blastx.14 | (AC007660) putative | gi 4895231 gb AAD3 | 45% | 23 | 439 |

| | | | | | RNA helicase [Arabidopsis thaliana] | 2817.1 AC007660_18 | 47% | 579 | 761 |
|---------|---------|-----|----------------|--|---|-------------------------------|-------|-----|-----|
| HWAAX38 | 943936 | 208 | HMMER 1.8 | | PFAM: Helicases conserved C-terminal domain | PF00271 | 34.57 | 48 | 221 |
| | | | blastx.2 | | PUTATIVE SNF2/SW12 FAMILY TRANSCRIPTION FACTOR. | sp Q9SHB2 Q9SHB2 | 46% | 39 | 380 |
| HMSFN70 | 1210794 | 209 | blastx.2 | | CDNA FLJ20421 FIS, CLONE KAT02467. | sp BAA91158 BAA9 1158 | 96% | 1 | 921 |
| HMSFN70 | 921879 | 763 | HMMER 2.1.1 | | PFAM: Inositol monophosphatase family | PF00459 | 40.2 | 703 | 795 |
| | | | blastx.14 | | (AL032655) predicted using Genefinder; similar to 1 this gene [Caenorhabditis elegans] | gi 3881275 emb CAA 21725.1 | 43% | 328 | 492 |
| | | | | | | | 52% | 703 | 822 |
| | | | | | | | 48% | 556 | 678 |
| | | | | | | | 24% | 25 | 273 |
| HUSGB93 | 1224029 | 210 | blastx.2 | | BISPHOSPHATE 3'- NUCLEOTIDASE. | sp O95861 O95861 | 99% | 426 | 953 |
| | | | | | | | 100% | 146 | 364 |
| HUSGB93 | 923014 | 764 | HMMER 1.8 | | PFAM: Inositol monophosphatase family | PF00459 | 33.91 | 125 | 388 |
| | | | blastx.14 | | (AF125042) bisphosphate 3-nucleotidase [Homo sapiens] | gi 4325316 gb AAD1 7329.1 | 100% | 17 | 493 |
| HELHL56 | 1164004 | 211 | blastx.2 | | CDNA FLJ11068 FIS, CLONE PLACE1004918, WEAKLY SIMILAR TO 1 | sp BAA91985 BAA9 1985 | 99% | 8 | 655 |
| HELHL56 | 578441 | 765 | HMMER 1.8 | | PFAM: L-lactate dehydrogenases | PF00056 | 33.17 | 80 | 211 |

| | | | | | | | | |
|---------|---------|-----|----------------|--|--------------------------|---------------------------|------------------------|-------------------------|
| HOENY85 | 1191756 | 212 | blastx.2 | CDNA FLJ11068 FIS, CLONE PLACE1004918, WEAKLY SIMILAR TO 1 | sp BAA91985 BAA9 1985 | 93% | 53 | 1069 |
| HOENY85 | 875830 | 766 | HMMER 1.8 | PFAM: L-lactate dehydrogenases | PF00056 | 144.25 | 38 | 598 |
| HTEHI14 | 1102680 | 213 | blastx.2 | LACTATE DEHYDROGENASE A (EC 1.1.1.27). | sp Q9XT87 Q9XT87 | 68% | 218 | 523 |
| HTEHI14 | 526687 | 767 | HMMER 2.1.1 | PFAM: lactate/malate dehydrogenase | PF00056 | 50.6 | 222 | 371 |
| HETDT70 | 1228235 | 214 | blastx.2 | NMD PROTEIN. | sp O95991 O95991 | 99% 52% | 25 540 | 558 596 |
| HETDT70 | 937999 | 768 | HMMER 2.1.1 | PFAM: Lipase | PF00151 | 125.4 | 139 | 528 |
| | | | blastx.2 | similar to the following EST sequences: GenBank Accession 1 sapiens] | gb AAC99994.1 | 88% 52% | 25 539 | 597 595 |
| HPIAT34 | 936262 | 215 | HMMER 2.1.1 | PFAM: Lipase | PF00151 | 123.9 | 305 | 535 |
| | | | blastx.2 | NMD PROTEIN. | sp O95991 O95991 | 80% 100% 92% 66% | 266 84 12 277 | 574 275 95 330 |
| HDPPO41 | 1204324 | 216 | blastx.2 | malate dehydrogenase (NAD+) (EC 1.1.1.-) precursor, mitochondrial - human | pir A39503 A39503 | 98% | 186 | 1937 |
| HDPPO41 | 963126 | 769 | HMMER 2.1.1 | PFAM: Malic enzyme | PF00390 | 243.6 | 258 | 572 |

| | | | | | | | | |
|---------|---------|-----|-------------|--|-------------------------|--|--|---|
| | | | blastx.14 | mitochondrial NAD(P) ⁺ -dependent malic enzyme [Homo sapiens] | gi 187300 gb AAA36197.1 | 99% | 186 | 569 |
| HMSHI83 | 1204709 | 217 | blastx.2 | malate dehydrogenase (NAD ⁺) (EC 1.1.1.-) precursor, mitochondrial - human | pir A39503 A39503 | 98% | 2 | 1720 |
| HMSHI83 | 963083 | 770 | HMMER 2.1.1 | PFAM: Malic enzyme | PF00390 | 621.6 | 41 | 751 |
| | | | blastx.14 | mitochondrial NAD(P) ⁺ -dependent malic enzyme [Homo sapiens] | gi 187300 gb AAA36197.1 | 96% 72% 43% | 2 753 855 | 784 785 902 |
| HTEPM45 | 952389 | 218 | HMMER 2.1.1 | PFAM: Malic enzyme | PF00390 | 924.1 | 33 | 1175 |
| | | | blastx.2 | malate dehydrogenase (NAD ⁺) (EC 1.1.1.-) precursor, mitochondrial - human | pir A39503 A39503 | 97% | 33 | 1229 |
| HTEPM45 | 953366 | 771 | HMMER 2.1.1 | PFAM: Fibrillar collagen C-terminal domain | PF01410 | 561.6 | 286 | 939 |
| | | | blastx.2 | prepro-alpha-1 type 3 collagen [Homo sapiens] | emb CAA32583.1 | 100% 59% 54% 54% 54% 53% 54% 48% 50% | 37 31 37 37 31 37 37 43 43 | 942 126 132 129 129 126 129 129 126 |
| HE8OV13 | 1228507 | 219 | blastx.2 | myosin heavy chain | pir S51823 S51823 | 44% | 33 | 923 |

| | | | | | | | | | |
|---------|---------|-----|-------------|--|--|---------------------------|-----------------------------|-------------------------|--------------------------|
| | | | | | ATM2 - Arabidopsis thaliana (fragment) | | 32% | 1263 | 1484 |
| HE8OV13 | 911341 | 772 | HMMER 1.8 | | PFAM: Myosin head (motor domain) (contains ATP/GTP binding P-loop) | PF00063 | 91.04 | 29 | 268 |
| | | | blastx.14 | | myr 6 myosin heavy chain [Rattus norvegicus] | gi 1575333 gb AAB38840.1 | 46% 40% 40% 32% | 41 617 608 449 | 274 742 697 559 |
| HELGU27 | 1011928 | 220 | blastx.2 | | MYOSIN I | sp Q63357 Q63357 | 93% 100% | 1 788 | 786 817 |
| HELGU27 | 923702 | 773 | HMMER 2.1.1 | | PFAM: Myosin head (motor domain) | PF00063 | 256.3 | 8 | 640 |
| | | | blastx.14 | | myosin I [Rattus norvegicus] | gi 3724141 emb CAA50871.1 | 97% 100% 100% 100% | 11 688 662 719 | 640 717 676 736 |
| HHEDC90 | 1226157 | 221 | blastx.2 | | MYOSIN I | sp Q63357 Q63357 | 57% | 216 | 3263 |
| HHEDC90 | 911447 | 774 | HMMER 2.1.1 | | PFAM: Myosin head (motor domain) | PF00063 | 241.2 | 25 | 597 |
| | | | blastx.14 | | myosin I [Rattus norvegicus] | gi 3724141 emb CAA50871.1 | 67% | 1 | 645 |
| HNBRB59 | 685902 | 222 | HMMER 1.8 | | PFAM: Myosin head (motor domain) (contains ATP/GTP binding P-loop) | PF00063 | 94.31 | 85 | 243 |
| | | | blastx.2 | | MYOSIN II NONMUSCLE (FRAGMENT) | sp Q91300 Q91300 | 92% | 85 | 246 |
| HNNBI16 | 965414 | 223 | HMMER 2.1.1 | | PFAM: Myosin head (motor domain) | PF00063 | 116.7 | 101 | 292 |

| | | | | | | | | |
|---------|---------|-----|----------------|--|-------------------------------|--------------------|--------------------|----------------------|
| HUJCL61 | 1223496 | 224 | blastx.2 | myosin I gamma, MMI gamma - mouse (fragment) | pir C45438 C45438 | 49% | 101 | 337 |
| | | | blastx.2 | MYOSIN I | sp Q63357 Q63357 | 59% 47% 41% | 159 2698 364 | 2717 3207 414 |
| HUJCL61 | 911432 | 776 | HMMER 2.1.1 | PFAM: Myosin head (motor domain) | PF00063 | 196 | 170 | 544 |
| | | | blastx.14 | myosin I [Rattus norvegicus] | gi 3724141 emb CAA 50871.1 | 72% 55% 81% | 140 604 534 | 532 750 599 |
| HWLRC68 | 1089187 | 225 | blastx.2 | Myosin X (Fragment). | sp AAF36524 AAF36 524 | 100% 92% 66% | 90 1238 1267 | 1238 1276 1302 |
| HWLRC68 | 911481 | 777 | HMMER 2.1.1 | PFAM: Myosin head (motor domain) | PF00063 | 97.7 | 222 | 485 |
| HFXFH42 | 713795 | 778 | HMMER 1.8 | PFAM: Neuraminidases | PF00064 | 9.26 | 259 | 354 |
| HEQAN73 | 958912 | 227 | HMMER 2.1.1 | PFAM: Phosphoglycerate mutase family | PF00300 | 64.2 | 87 | 359 |
| | | | blastx.2 | Hypothetical 30.1 kDa protein. | sp CAC01127 CAC0 1127 | 99% | 69 | 878 |
| HSLFS31 | 1106294 | 228 | blastx.2 | right oriC-binding protein - Escherichia coli | pir JU0158 JU0158 | 99% | 566 | 252 |
| HSLFS31 | 921511 | 779 | HMMER 2.1.1 | PFAM: Phosphoglycerate mutase family | PF00300 | 71.6 | 12 | 149 |
| | | | blastx.14 | Kenn Rudd identifies as gpmB [Escherichia coli] | gi 537235 gb AAA97 291.1 | 96% 100% | 3 188 | 188 223 |
| HELGK56 | 1103702 | 229 | blastx.2 | pyruvate kinase (EC 2.7.1.40) A - Escherichia | pir S29790 S29790 | 96% 63% | 572 619 | 96 554 |

| | | | | | | | | |
|---------|---------|-----|----------------|---|-----------------------------|---------------------|------------------|-------------------|
| HELGK56 | 925698 | 780 | HMMER 2.1.1 | coli PFAM: Pyruvate kinase | PF00224 | 406.9 | 147 | 731 |
| | | | blastx.14 | pyruvate kinase type II [Escherichia coli] | gi 147459 gb AAA24 473.1 | 98% 65% | 147 21 | 731 107 |
| HAMFW05 | 957586 | 230 | HMMER 1.8 | PFAM: Proyl oligopeptidase family | PF00326 | 33.83 | 1 | 174 |
| | | | blastx.2 | R26984.1 (FRAGMENT). | sp O75273 O75273 | 95% | 1 | 558 |
| HTEDG81 | 1193054 | 231 | blastx.2 | ALPHA 4 SUBUNIT OF 20S PROTEASOME. | sp Q9PTW9 Q9PTW 9 | 89% | 79 | 771 |
| HTEDG81 | 772995 | 781 | HMMER 2.1.1 | PFAM: Proteasome A- type and B-type | PF00227 | 114.6 | 180 | 488 |
| HAMGO24 | 943287 | 232 | HMMER 2.1.1 | PFAM: Ribonucleotide reductases | PF00268 | 316.2 | 2 | 490 |
| | | | blastx.2 | hypothetical protein DKFZp761E1312.1 - human (fragment) | pir T46249 T46249 | 90% | 2 | 550 |
| HMWBH91 | 1193044 | 233 | blastx.2 | house-keeping protein - mouse | pir S27870 S27870 | 53% 52% | 282 121 | 1295 279 |
| HMWBH91 | 882083 | 782 | HMMER 1.8 | PFAM: Ribosomal RNA adenine dimethylases | PF00398 | 23.82 | 385 | 921 |
| HOECH19 | 965639 | 234 | HMMER 1.8 | PFAM: Ribosomal RNA adenine dimethylases | PF00398 | 116.68 | 173 | 934 |
| | | | blastx.2 | CGI-75 PROTEIN. | sp Q9Y384 Q9Y384 | 95% 100% 100% | 140 72 911 | 853 161 934 |
| HSRAA80 | 1121919 | 235 | blastx.2 | POLYMERASE (FRAGMENT). | sp Q9UQG0 Q9UQG 0 | 63% 39% | 17 421 | 361 498 |
| HSRAA80 | 937640 | 783 | HMMER | PFAM: Reverse | PF00078 | 20.88 | 11 | 130 |

| | | | | | | | | | |
|---------|---------|-----|-----------|--|--------------------------|-------------------|-----------------|---------------|--|
| | | | 1.8 | transcriptase (RNA-dependent DNA polymerase) | | | | | |
| | | | blastx.14 | (AF080232) polymerase [Human endogenous retrovirus K] | gi 3600069 gb AAC63292.1 | 65% | 17 | 325 | |
| HHEDF50 | 1174682 | 236 | blastx.2 | nitrogen regulation protein II (EC 2.7.3.-) ntrB - Escherichia coli | pir A30377 RGECGL | 89% | 44 | 490 | |
| HHEDF50 | 974396 | 784 | HMMER 1.8 | PFAM: Signal C terminal domain | PF00512 | 115.35 | 65 | 490 | |
| | | | blastx.14 | NR(II) (glnL gene product) (AA 1-349) [Escherichia coli] | gi 41564 emb CAA28807.1 | 100% | 86 | 427 | |
| HHMK34 | 974395 | 237 | HMMER 1.8 | PFAM: Signal C terminal domain | PF00512 | 62.83 | 56 | 277 | |
| | | | blastx.2 | nitrogen regulation protein II (EC 2.7.3.-) ntrB - Escherichia coli | pir A30377 RGECGL | 78% | 50 | 415 | |
| HMAGK69 | 1105451 | 238 | blastx.2 | hypothetical 60.6 kD protein in deub-lysu intergenic region - Escherichia coli (strain K-12) | pir D65222 D65222 | 96% 100% | 523 618 | 26 523 | |
| HMAGK69 | 723186 | 785 | HMMER 1.8 | PFAM: Signal C terminal domain | PF00512 | 40.87 | 31 | 405 | |
| HNGNW52 | 1132300 | 239 | blastx.2 | protein-histidine kinase (EC 2.7.3.-) - Escherichia coli | pir G64840 G64840 | 93% 80% 90% | 939 86 37 | 55 42 5 | |
| HNGNW52 | 883074 | 786 | HMMER | PFAM: Signal C terminal | PF00512 | 174.7 | 464 | 997 | |

| | | | 1.8 | domain | | | | |
|---------|---------|-----|----------------|---|--------------------------|-------|-----|------|
| H6EDK67 | 974775 | 240 | HMMER 2.1.1 | PFAM: Signal peptidase I | PF00461 | 218.3 | 165 | 641 |
| | | | blastx.2 | signal peptidase (EC 3.4.99.-) 21K chain - dog | pir A34229 A34229 | 98% | 93 | 668 |
| HWBCS43 | 1151532 | 241 | blastx.2 | signal peptidase (EC 3.4.99.-) 18K chain - dog | pir A35309 A35309 | 93% | 344 | 880 |
| HWBCS43 | 772564 | 787 | HMMER 2.1.1 | PFAM: Signal peptidase I | PF00461 | 117.2 | 381 | 653 |
| HCE3H71 | 961681 | 242 | HMMER 2.1.1 | PFAM: Sushi domain (SCR repeat) | PF00084 | 79.2 | 317 | 496 |
| | | | blastx.2 | seizure-related protein SEZ-6 precursor - mouse | pir 52657 52657 | 83% | 5 | 685 |
| | | | | | | 64% | 565 | 957 |
| | | | | | | 30% | 98 | 496 |
| | | | | | | 48% | 929 | 1000 |
| HOFMS43 | 947973 | 243 | HMMER 2.1.1 | PFAM: Sushi domain (SCR repeat) | PF00084 | 64 | 174 | 302 |
| | | | blastx.2 | PORCINE MEMBRANE COFACTOR PROTEIN. | sp O02839 O02839 | 47% | 12 | 317 |
| HOVCO14 | 947999 | 244 | HMMER 2.1.1 | PFAM: Sushi domain (SCR repeat) | PF00084 | 84 | 21 | 170 |
| | | | blastx.2 | UNKNOWN PROTEIN (FRAGMENT). | sp Q28797 Q28797 | 33% | 21 | 347 |
| | | | | | | 34% | 21 | 380 |
| | | | | | | 38% | 424 | 516 |
| | | | | | | 47% | 424 | 474 |
| HTOBE75 | 1161571 | 245 | blastx.2 | P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) 1-MOLECULE 3) | sp P16109 LEM3_H UMAN | 95% | 3 | 1067 |
| | | | | | | 38% | 3 | 878 |
| | | | | | | 37% | 3 | 866 |
| | | | | | | 35% | 3 | 863 |
| | | | | | | 34% | 3 | 866 |

| | | | | | | | | |
|---------|---------|-----|-----------------------------|--|--|----------------------------|--------------------------|--------------------------|
| HTOBE75 | 591896 | 788 | HMMER 2.1.1 | (LECAM3). PFAM: Sushi domain (SCR repeat) | PF00084 | 39% | 48 | 866 |
| HCM5L08 | 898203 | 246 | HMMER 2.1.1 blastx.2 | PFAM: Calsequestrin calsequestrin precursor, fast skeletal muscle - human | PF01216 pir A60424 A60424 | 1001.1 95% | 52 112 | 1221 1197 |
| HCM5L08 | 959176 | 789 | HMMER 2.1.1 blastx.14 | PFAM: Calsequestrin calmitine; calsequestrine [Homo sapiens] | PF01216 gi 688292 gb AAB32 063.1 | 697.4 93% | 1372 | 569 593 |
| HDPBS64 | 846624 | 247 | HMMER 1.8 blastx.2 | PFAM: Thioredoxins ZK973.11 protein. | PF00085 sp AAF40013 AAF40 013 | 116.87 32% | 173 182 | 493 652 |
| HDTBR50 | 846630 | 248 | HMMER 1.8 blastx.2 | PFAM: Thioredoxins NM23-H8. | PF00085 sp AAF20909 AAF20 909 | 29.85 100% 97% | 163 130 327 | 297 327 467 |
| HTDAB17 | 890384 | 249 | HMMER 2.1.1 blastx.2 | PFAM: Thioredoxin CG1837 PROTEIN. | PF00085 sp Q9VYV3 Q9VYV 3 | 107.9 42% 43% 41% | 276 225 231 348 | 533 518 539 533 |
| HABAE22 | 1227053 | 250 | blastx.2 | CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN. | sp Q9UNE7 Q9UNE7 | 95% | 169 | 1023 |
| HABAE22 | 965314 | 790 | HMMER | PFAM: TPR Domain | PF00515 | 38.4 | 300 | 383 |

| | | | | | | | | |
|---------|---------|-----|-------------|---|--------------------------|-------------------|-----------------|-------------------|
| | | | 2.1.1 | (AF039689) antigen NY-CO-7 [Homo sapiens] | gi 3170178 gb AAC18038.1 | 92% | 171 | 725 |
| HE9MI70 | 1217048 | 251 | blastx.2 | UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 25 (EC 3.1.2.15) 1 PROTEASE 25) | sp P57080 UBPP_MOUSE | 52% | 15 | 758 |
| HE9MI70 | 953319 | 791 | HMMER 1.8 | (DEUBIQUITINATING ENZYME 25). | PF00515 | 16.42 | 154 | 240 |
| HHFDK15 | 854734 | 792 | HMMER 2.1.1 | PFAM: TPR Domain | PF00515 | 21.7 | 213 | 299 |
| HOSNZ11 | 1162664 | 253 | blastx.2 | conserved hypothetical protein MTH68 - Methanobacterium 1 | pir E69190 E69190 | 36% | 134 | 448 |
| HOSNZ11 | 965875 | 793 | HMMER 2.1.1 | PFAM: TPR Domain | PF00515 | 30.3 | 144 | 230 |
| | | | blastx.14 | (AE000798) O-linked GlcNAc transferase [Methanobacterium thermoautotrophicum] | gi 2621106 gb AAB84576.1 | 34% 23% 36% | 249 3 395 | 362 236 484 |
| HTAEW05 | 1151514 | 254 | blastx.2 | DJ979N1.1 (DJ979N1.1). | sp Q9UGR2 Q9UGR2 | 100% | 215 | 658 |
| HTAEW05 | 838562 | 794 | HMMER 1.8 | PFAM: TPR Domain | PF00515 | 16.51 | 460 | 546 |
| HTTKN45 | 1181807 | 255 | blastx.2 | BCDNA:GH04929 PROTEIN. | sp Q9V3G6 Q9V3G6 | 23% | 420 | 1583 |

| | | | | | | | | |
|---------|---------|-----|-----------------------------|--|-------------------------------|-------|------|------|
| HTTKN45 | 914589 | 795 | HMMER 1.8 blastx.14 | PFAM: TPR Domain (AF181631) BcDNA.GH04929 [Drosophila melanogaster] | PF00515 | 18.74 | 383 | 469 |
| HUSJN62 | 923146 | 256 | HMMER 2.1.1 blastx.2 | PFAM: TPR Domain CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN. | sp Q9UNE7 Q9UNE7 | 94% | 1189 | 353 |
| HTEIU92 | 1102681 | 257 | blastx.2 | Transketolase (EC 2.2.1.1). | sp AAF76194 AAF76 194 | 71% | 1 | 564 |
| HTEIU92 | 870652 | 796 | HMMER 2.1.1 blastx.2 | PFAM: Transketolase | PF00456 | 70.1 | 1 | 225 |
| HAQMD86 | 1105267 | 258 | blastx.2 | UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 10 (EC 3.1.2.15) 1 1 | sp Q14694 UBPA_H UMAN | 96% | 13 | 1878 |
| HAQMD86 | 961459 | 797 | HMMER 2.1.1 blastx.14 | PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 similar to ubiquitin- specific proteinase of S.cerevisiae. [Homo sapiens] | PF00443 | 89.1 | 1700 | 1900 |
| HBJJG02 | 1151462 | 259 | blastx.2 | CG5794 PROTEIN. | gi 1136438 dbj BAA1 1507.1 | 96% | 2 | 1879 |
| HBJJG02 | 919508 | 798 | HMMER 2.1.1 | PFAM: Ubiquitin carboxyl-terminal | sp Q9VC56 Q9VC56 PF00443 | 48% | 795 | 1409 |
| | | | | | | 80.6 | 176 | 460 |

| | | | | | | | | | |
|---------|---------|-----|-----------------------------|--|--------------------------|-------------------------------|--|---|--|
| HBJN65 | 1151463 | 260 | blastx.2 | UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 25 (EC 3.1.2.15) 1 PROTEASE 25) (DEUBIQUITINATING ENZYME 25). | sp P57080 UBPP_M OUSE | gi 1666075 emb CAA 66942.1 | 56% 26% 55% 25% 25% 46% 31% 22% | 164 314 50 485 626 281 821 188 | 253 481 103 613 709 319 886 268 |
| HBJN65 | 960507 | 799 | HMMER 2.1.1 blastx.14 | PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 similar to ubiquitin carboxyl-terminal hydrolase; 1 1 cDNA EST EMBL:D64405 comes from this gene; cDNA EST EMBL:D68146 | PF00443 | gi 3878110 emb CAA 87786.1 | 80.5 40% 40% | 514 409 607 | 723 588 681 |
| HBMUJ35 | 1195500 | 261 | blastx.2 | UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 23 (EC | sp Q9UK80 UBPN_H UMAN | | 91% | 1982 | 288 |

| | | | | | | | | |
|---------|---------|-----|-----------------------------|---|-----------------------------|-------------|--------------|--------------|
| HBMUJ35 | 956041 | 800 | HMMER 2.1.1 blastx.14 | 3.1.2.15)11 PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 (AF177758) ubiquitin specific protease 16 [Homo sapiens] | PF00443 | 54.6 | 492 | 355 |
| HCEBP60 | 1227635 | 262 | blastx.2 | LSFR3 PROTEIN (FRAGMENT). | sp Q9W6U5 Q9W6U 5 | 85% 75% | 1737 2863 | 2846 2910 |
| HCEBP60 | 812297 | 801 | HMMER 1.8 | PFAM: Ubiquitin carboxyl-terminal hydrolases family 2 | PF00443 | 59.49 | 168 | 281 |
| HFGMA55 | 1150870 | 263 | blastx.2 | UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 23 (EC 3.1.2.15)11 | sp Q9UK80 UBPN_H UMAN | 100% | 10 | 444 |
| HFGMA55 | 858681 | 802 | HMMER 2.1.1 | PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 | PF00443 | 57.8 | 237 | 377 |
| HLHTE91 | 789603 | 264 | HMMER 2.1.1 blastx.2 | PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 DEUBIQUITINATING ENZYME. | PF00443 sp Q9UNP0 Q9UNP0 | 92.4 40% | 862 409 | 1068 1077 |
| HLHTE91 | 868803 | 803 | HMMER 2.1.1 | PFAM: MYND finger | PF01753 | 33.7 | 393 | 521 |
| HLYFI58 | 1151495 | 265 | blastx.2 | UBIQUITIN CARBOXYL- TERMINAL | sp Q9Y5T5 UBPG_H UMAN | 100% | 2 | 625 |

| | | | | | | | | |
|---------|---------|-----|----------------|--|-------------------------------|--|--|--|
| HLFYI58 | 924193 | 805 | HMMER 2.1.1 | HYDROLASE 16 (EC 3.1.2.15) 1 1 1 | PF00443 | 77.4 | 368 | 619 |
| | | | blastx.14 | PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 (AF126736) ubiquitin processing protease [Homo sapiens] | gi 4454565 gb AAD2 0949.1 | 100% | 2 | 625 |
| HNNBJ44 | 915273 | 806 | HMMER 2.1.1 | HYDROLASE 16 (EC 3.1.2.15) 1 1 1 | PF00443 | 50.1 | 1045 | 1131 |
| | | | blastx.14 | PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 similar to ubiquitin carboxyl-terminal hydrolase; 1 1 cDNA EST EMBL:D34547 comes from this gene; cDNA EST EMBL:D37684 | gi 3879501 emb CAA 87795.1 | 44% 28% 42% 35% 23% 72% | 688 292 1276 1093 1961 1057 | 915 462 1332 1134 2062 1089 |
| HSLJI46 | 997643 | 267 | blastx.2 | UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 8 (EC 3.1.2.15) 1 1 | sp P40818 UBP8_HU MAN | 82% 100% 79% | 64 1 510 | 498 87 596 |
| HSLJI46 | 883028 | 807 | HMMER 2.1.1 | PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 | PF00443 | 99.8 | 1336 | 1521 |
| HTFOK70 | 1151518 | 268 | blastx.2 | CG3016 PROTEIN. | sp Q9W462 Q9W462 | 56% 41% 63.6 | 361 16 359 | 561 153 568 |
| HTFOK70 | 914561 | 808 | HMMER 2.1.1 | PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 | PF00443 | | | |

| | | | | | | | | |
|---------|---------|-----|----------------|--|------------------------------|------------|----------|------------|
| | | | blastx.14 | (AC003974) putative ubiquitin specific protease [Arabidopsis thaliana] | gi 2914695 gb AAC0 4485.1 | 60% | 473 | 571 |
| HUSXO71 | 1164014 | 269 | blastx.2 | UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 18 (EC 3.1.2.15) 1 1 1 | sp Q9UMW8 UBPL_ HUMAN | 39% 37% | 7 368 | 129 472 |
| HUSXO71 | 862649 | 809 | HMMER 2.1.1 | PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 | PF00443 | 100% | 400 | 480 |
| HWBDP39 | 1223498 | 270 | blastx.2 | CDNA FLJ20314 FIS, CLONE HEP07831. | sp BAA91084 BAA9 1084 | 88% | 1313 | 2239 |
| HWBDP39 | 810403 | 810 | HMMER 2.1.1 | PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 | PF00443 | 55.2 | 227 | 382 |
| HKMMQ73 | 840459 | 271 | HMMER 1.8 | PFAM: UDP- glucuronosyl and UDP- glucosyl transferases | PF00201 | 93.48 | 28 | 327 |
| | | | blastx.2 | 2-hydroxyacylsphingosine 1-beta- galactosyltransferase (EC 1 | pir JC5423 JC5423 | 88% | 7 | 417 |
| HVVVK72 | 1179755 | 272 | blastx.2 | glucuronosyltransferase (EC 2.4.1.17) UGT2B13 precursor - rabbit | pir B47113 B47113 | 35% | 69 | 461 |
| HVVVK72 | 933167 | 812 | HMMER 1.8 | PFAM: UDP- glucuronosyl and UDP- glucosyl transferases | PF00201 | 70.01 | 2 | 391 |
| H7TXB52 | 981972 | 273 | blastx.2 | DUAL SPECIFICITY | sp Q9UNI6 DUSC_H | 100% | 303 | 1322 |

| | | | | PROTEIN PHOSPHATASE 12 (EC 3.1.3.48) (EC 1 | UMAN | | | |
|---------|---------|-----|----------------|---|-------------------------------|--------------------------|----------------------------|-----------------------------|
| H7TXB52 | 910910 | 813 | HMMER 2.1.1 | PFAM: Dual specificity phosphatase, catalytic domain | PF00782 | 117.9 | 378 | 806 |
| | | | blastx.14 | (AB004537) PROTEIN- TYROSINE PHOSPHATASE YVH1 [Schizosaccharomyces pombe] | gi 2257526 dbj BAA2 1420.1 | 26% 48% 52% 38% | 516 1143 1092 960 | 968 1292 1142 1013 |
| HDPY71 | 1217205 | 274 | blastx.2 | Mitogen-activated protein kinase phosphatase x. | sp AAF86649 AAF86 649 | 99% 100% | 531 392 | 848 529 |
| HDPY71 | 971345 | 814 | HMMER 2.1.1 | PFAM: Dual specificity phosphatase, catalytic domain | PF00782 | 109.1 | 492 | 719 |
| | | | blastx.14 | DsPTP1 protein [Arabidopsis thaliana] | gi 4150963 emb CAA 77232.1 | 48% 43% | 492 377 | 716 487 |
| HGOCA12 | 968763 | 275 | HMMER 2.1.1 | PFAM: Dual specificity phosphatase, catalytic domain | PF00782 | 28.6 | 112 | 360 |
| | | | blastx.2 | PROTEIN PHOSPHATASE. | sp Q9UII6 Q9UII6 | 40% | 25 | 360 |
| HGOCA12 | 971583 | 815 | HMMER 2.1.1 | PFAM: Dual specificity phosphatase, catalytic domain | PF00782 | 60.1 | 467 | 318 |
| | | | blastx.14 | phosphatase tyrosine/serine [Homo sapiens] | gi 181840 gb AAA35 777.1 | 48% | 515 | 318 |
| HHCJ29 | 1077517 | 276 | blastx.2 | hypothetical protein | pir T14756 T14756 | 100% | 490 | 1716 |

[illegible]

| | | | | | | | | |
|---------|---------|-----|----------------|---|--------------------------|---------------------------|------------------------|--------------------------|
| HMIAO23 | 675329 | 819 | HMMER 2.1.1 | INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1. | PF00043 | 29.5 | 23 | 184 |
| HELDW45 | 944301 | 282 | HMMER 2.1.1 | PFAM: Glutathione S- transferases. | PF00408 | 133.1 | 114 | 512 |
| | | | blastx.2 | Phosphoglucosyltransferase/phosphomannomutase | pir G64803 G64803 | 99% | 3 | 512 |
| HSRBB31 | 1121889 | 283 | blastx.2 | phosphoglucosyltransferase (EC 5.4.2.2) - Escherichia coli | sp BAA99407 BAA9 9407 | 100% 64% 54% 71% | 3 493 395 707 | 440 861 526 790 |
| HSRBB31 | 958210 | 820 | HMMER 1.8 | 3-methylcrotonyl-CoA carboxylase biotin- containing 1 | PF00364 | 75.97 | 1455 | 1643 |
| HTEOW39 | 1151517 | 284 | blastx.2 | PFAM: Biotin-requiring enzymes | pir JE0185 JE0185 | 49% | 65 | 484 |
| HTEOW39 | 870566 | 821 | HMMER 1.8 | lysozyme (EC 3.2.1.17) - bare-faced crassow | PF00062 | 126.92 | 59 | 295 |
| HE2PE32 | 1106571 | 285 | blastx.2 | PFAM: C-type lysozymes and alpha-lactalbumin | pir B65175 B65175 | 85% | 1 | 540 |
| HE2PE32 | 524511 | 822 | HMMER 1.8 | 6-phospho-beta- glucosidase (EC 3.2.1.86) bg B - Escherichia coli | PF00232 | 87.26 | 17 | 289 |
| HSIDW39 | 1211446 | 286 | blastx.2 | PFAM: Glycosyl hydrolases family 1 | sp CAC08178 CAC0 8178 | 99% | 56 | 748 |
| HSIDW39 | 775139 | 823 | HMMER 2.1.1 | Cytosolic beta- glucosidase (Fragment). | PF00232 | 134 | 28 | 372 |

| | | | | | | | | |
|---------|---------|-----|----------------|--|-------------------------------|---|--|---|
| | | | blastx.2 | cytosolic beta-glucosidase [Cavia porcellus] | gb AAB41058.1 | 84% | 1 | 363 |
| HSIDW39 | 830774 | 824 | HMMER 2.1.1 | PFAM: Glycosyl hydrolase family 1 | PF00232 | 155.5 | 42 | 419 |
| HPMLD30 | 1226192 | 287 | blastx.2 | alpha-glucosidase (EC 3.2.1.20) - Escherichia coli | pir C64769 C64769 | 96% | 44 | 1543 |
| HPMLD30 | 937414 | 825 | HMMER 1.8 | PFAM: Alpha amylases (family of glycosyl hydrolases) | PF00128 | 18.21 | 402 | 479 |
| | | | blastx.2 | maltodextrin glucosidase [Escherichia coli] | gb AAB40159.1 | 99% | 30 | 485 |
| HOEKP17 | 1204712 | 288 | blastx.2 | FLAVOHEMOPROTEIN B5+B5R. | sp Q9UHI9 Q9UHI9 | 90% 97% | 749 214 | 1675 870 |
| HOEKP17 | 931049 | 826 | HMMER 2.1.1 | PFAM: Heme-binding domain in cytochrome b5 and oxidoreductases | PF00173 | 69.6 | 258 | 428 |
| | | | blastx.14 | (AL032654) similar to Heme-binding domain in 1 | gi 3881161 emb CAA 21721.1 | 60% 35% 36% 60% 50% 39% 57% 55% 45% | 261 1118 906 156 1253 1565 1352 1055 580 | 473 1285 1013 215 1318 1648 1393 1081 639 |
| HFXDP67 | 1228141 | 289 | blastx.2 | hypothetical protein b0872 - Escherichia coli | pir H64825 H64825 | 95% | 240 | 1205 |
| HFXDP67 | 526951 | 827 | HMMER 1.8 | PFAM: FAD/NAD- binding domain in | PF00175 | 13.6 | 293 | 415 |

| | | | | | | | | |
|---------|---------|-----|-------------|---|--------------------------|-------------------|----------------|-----------------|
| HJABA59 | 1199933 | 290 | blastx.2 | oxidoreductases | sp Q9UBK8 Q9UBK8 | 91% | 2 | 904 |
| HJABA59 | 713642 | 828 | HMMER 1.8 | PFAM: FAD/NAD-binding domain in oxidoreductases | PF00175 | 100.6 | 423 | 797 |
| HKIXB03 | 1129055 | 291 | blastx.2 | CYTOCHROME B5 REDUCTASE B5R.2. | sp Q9UHI0 Q9UHI0 | 93% 82% 88% | 197 2 70 | 370 88 96 |
| HKIXB03 | 924636 | 829 | HMMER 1.8 | PFAM: FAD/NAD-binding domain in oxidoreductases | PF00175 | 31.48 | 192 | 326 |
| | | | blastx.2 | (AL133582) hypothetical protein [Homo sapiens] | emb CAB63726.1 | 85% | 144 | 371 |
| HKMMF49 | 1124742 | 292 | blastx.2 | Kidney superoxide-producing NADPH oxidase. | sp BAA95695 BAA95695 | 100% | 10 | 600 |
| HKMMF49 | 677960 | 830 | HMMER 2.1.1 | PFAM: Ferric reductase like transmembrane component | PF01794 | 63.6 | 79 | 294 |
| HLD0G51 | 1151491 | 293 | blastx.2 | Neurospora crassa hypothetical protein 15E6.170 - Neurospora crassa | pir T48809 T48809 | 40% 32% | 163 654 | 522 800 |
| HLD0G51 | 918840 | 831 | HMMER 2.1.1 | PFAM: Oxidoreductase FAD/NAD-binding domain | PF00175 | 62.6 | 524 | 904 |
| | | | blastx.14 | phenolhydroxylase component [Acinetobacter] | gi 535285 emb CAA85385.1 | 32% 36% | 269 860 | 370 967 |

| | | | | | | | | | |
|---------|---------|-----|-------------|--|---------------------------|--|-------|------|------|
| HSVAI25 | 1130819 | 294 | blastx.2 | calcoaceticus] | | | 37% | 647 | 727 |
| | | | | Hypothetical 12.9 kDa protein. | sp BAB12124 BAB12124 | | 42% | 527 | 583 |
| HSVAI25 | 577154 | 832 | HMMER 1.8 | PFAM: FAD/NAD-binding domain in oxidoreductases | PF00175 | | 44% | 215 | 268 |
| | | | | | | | 58% | 524 | 652 |
| | | | | | | | 66% | 663 | 761 |
| HSXCP56 | 924635 | 295 | HMMER 2.1.1 | PFAM: FAD/NAD-binding Cytochrome reductase | PF00970 | | 7.34 | 126 | 212 |
| | | | | | | | 162.3 | 243 | 500 |
| | | | blastx.2 | CYTOCHROME B5 REDUCTASE B5R.2. | sp Q9UHHJ Q9UHHJ0 | | 91% | 171 | 950 |
| | | | | | | | 100% | 142 | 240 |
| HBCAT08 | 1167275 | 296 | blastx.2 | PXN PROTEIN. | sp Q9VZZ4 Q9VZZ4 | | 49% | 71 | 2419 |
| | | | | | | | 37% | 2237 | 2461 |
| | | | | | | | 50% | 3295 | 3351 |
| | | | | | | | 36% | 157 | 246 |
| HBCAT08 | 920940 | 833 | HMMER 1.8 | PFAM: Peroxidases | PF00141 | | 32.87 | 3 | 347 |
| | | | blastx.14 | similar to D.melanogaster peroxidase(U11052) [Homo sapiens] | gi 1504040 dbj BAA13219.1 | | 92% | 183 | 347 |
| | | | | | | | 93% | 3 | 134 |
| | | | | | | | 92% | 160 | 198 |
| | | | | | | | 29% | 133 | 183 |
| HHFBU53 | 1048855 | 297 | blastx.2 | subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A - human | pir A39490 A39490 | | 85% | 4 | 570 |
| | | | | | | | | | |
| HHFBU53 | 837647 | 834 | HMMER 2.1.1 | PFAM: Proprotein convertase P-domain | PF01483 | | 254.1 | 381 | 797 |
| | | | | | | | | | |
| HTTDO45 | 942505 | 298 | HMMER | PFAM: Thiolase | PF00108 | | 794.8 | 459 | 1637 |

| | | | | | | | | | | |
|---------|---------|-----|-------------|--|--|--------------------------|--|--------|------|------|
| | | | 2.1.1 | | 3-oxoacyl-CoA thiolase - human | pir S43440 S43440 | | | 456 | 1640 |
| HTPII72 | 1104236 | 299 | blastx.2 | | valine--tRNA ligase (EC 6.1.1.9) - rat (fragment) | pir PN0473 PN0473 | | 92% | 4 | 657 |
| HTPII72 | 958035 | 835 | HMMER 1.8 | | PFAM: tRNA synthetases class I | PF00133 | | 280.02 | 4 | 645 |
| | | | blastx.14 | | transfer RNA-Val synthetase [Rattus norvegicus] | gi 207625 gb AAA42320.1 | | 56% | 4 | 576 |
| H6BSE22 | 1151371 | 300 | blastx.2 | | UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (EC 3.1.2.15) 1 1 1 | sp Q9Y5T5 UBPG_HUMAN | | 51% | 589 | 750 |
| | | | | | | | | 58% | 780 | 866 |
| | | | | | | | | 99% | 156 | 623 |
| H6BSE22 | 969019 | 836 | HMMER 2.1.1 | | PFAM: Ubiquitin carboxyl-terminal hydrolases family 2 | PF00442 | | 41.8 | 738 | 833 |
| | | | blastx.14 | | (AF126736) ubiquitin processing protease [Homo sapiens] | gi 4454565 gb AAD20949.1 | | 94% | 672 | 1493 |
| | | | | | | | | 100% | 156 | 602 |
| | | | | | | | | 94% | 1482 | 1538 |
| | | | | | | | | 100% | 1573 | 1599 |
| | | | | | | | | 42% | 1452 | 1514 |
| | | | | | | | | 50% | 781 | 810 |
| HDPAB43 | 1220621 | 301 | blastx.2 | | Ubiquitin specific protease (Fragment). | sp AAF66953 AAF66953 | | 80% | 114 | 1586 |
| HDPAB43 | 864998 | 837 | HMMER 2.1.1 | | PFAM: Ubiquitin carboxyl-terminal hydrolases family 2 | PF00442 | | 63.9 | 236 | 331 |
| HDPFM16 | 1193042 | 302 | blastx.2 | | CG8830 PROTEIN. | sp Q9V6C0 Q9V6C0 | | 53% | 180 | 470 |

| | | | | | | | | |
|---------|---------|-----|----------------|--|-------------------------------|-------|------|------|
| HDPFM16 | 810401 | 838 | HMMER 2.1.1 | PFAM: Ubiquitin carboxyl-terminal hydrolases family 2 | PF00442 | 50% | 983 | 1201 |
| | | | | | | 30% | 1571 | 1828 |
| | | | | | | 41% | 611 | 778 |
| | | | | | | 41% | 1319 | 1435 |
| HFPCN10 | 1151478 | 303 | blastx.2 | CDNA FLJ10809 FIS, CLONE NT2RP4000927, WEAKLY SIMILAR TO 1.1 | sp BAA91825 BAA9 1825 | 62 | 163 | 258 |
| | | | | | | 69% | 330 | 518 |
| HFPCN10 | 915568 | 839 | HMMER 1.8 | PFAM: Ubiquitin carboxyl-terminal hydrolases family 2 | PF00442 | 32.31 | 417 | 470 |
| | | | blastx.14 | (AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe] | gi 3560166 emb CAA 20678.1 | 50% | 345 | 464 |
| | | | | | | 33% | 466 | 555 |
| HLQFO35 | 933901 | 840 | HMMER 1.8 | PFAM: Ubiquitin carboxyl-terminal hydrolases family 2 | PF00442 | 11.44 | 131 | 181 |
| HMWJU94 | 1150834 | 305 | blastx.2 | UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 12 (EC 3.1.2.15) 1.1.1 | sp O75317 UBPC_H UMAN | 92% | 162 | 536 |
| HMWJU94 | 705880 | 841 | HMMER 2.1.1 | PFAM: Ubiquitin carboxyl-terminal hydrolases family 2 | PF00442 | 58.8 | 231 | 326 |

| | | | | | | | | |
|---------|---------|-----|-------------|---|--------------------------|--------|------|------|
| HSATQ28 | 1124600 | 306 | blastx.2 | PRO0758. | sp AAF71030 AAF71030 | 86% | 222 | 491 |
| HSATQ28 | 866951 | 842 | HMMER 1.8 | PFAM: Ubiquitin carboxyl-terminal hydrolases family 2 | PF00442 | 11.1 | 90 | 122 |
| HTPIL46 | 1196787 | 307 | blastx.2 | Cyld protein. | sp CAB93333 CAB93333 | 99% | 963 | 1859 |
| | | | | | | 99% | 246 | 962 |
| | | | | | | 99% | 1870 | 2265 |
| | | | | | | 37% | 669 | 842 |
| | | | | | | 37% | 1596 | 1754 |
| HTPIL46 | 973570 | 843 | HMMER 2.1.1 | PFAM: CAP-Gly domain | PF01302 | 28.2 | 872 | 955 |
| | | | blastx.2 | (AF161542) HSPC057 [Homo sapiens] | gb AAF29029.1 AF161542_1 | 93% | 626 | 2167 |
| | | | | | | 100% | 2143 | 2169 |
| | | | | | | 45% | 512 | 577 |
| HNGEN37 | 1103305 | 308 | blastx.2 | indole-3-glycerol-phosphate synthase (EC 4.1.1.48) / 1 coli | pir A64874 GWEC | 99% | 1 | 531 |
| HNGEN37 | 663955 | 844 | HMMER 2.1.1 | PFAM: Indole-3-glycerol phosphate synthases | PF00218 | 125.4 | 2 | 223 |
| HLMDO77 | 974855 | 309 | HMMER 1.8 | PFAM: Trypsin | PF00089 | 114.97 | 116 | 523 |
| | | | blastx.2 | Complement C1r-like proteinase precursor. | sp AAF44349 AAF44349 | 100% | 116 | 547 |
| HNKAZ51 | 1154961 | 310 | blastx.2 | SERINE PROTEASE DESC1. | sp Q9UL52 Q9UL52 | 48% | 100 | 957 |
| HNKAZ51 | 947067 | 846 | HMMER 1.8 | PFAM: Trypsin | PF00089 | 124.58 | 259 | 594 |
| | | | blastx.2 | (AF064819) serine protease DESC1 [Homo | gb AAF04328.1 AF064819_1 | 42% | 100 | 603 |
| | | | | | | 35% | 677 | 832 |

| | | | | | | | | |
|---------|--------|-----|--------------------------|--------------------------------------|-----------------------------|--------|-----|------|
| HOGDR01 | 919899 | 311 | HMMER 1.8 | sapiens] PFAM: Trypsin | PF00089 | 46% | 603 | 686 |
| HOGDR01 | 947085 | 847 | blastx.2 HMMER 1.8 | SP001LA (FRAGMENT). PFAM: Trypsin | sp O43342 O43342 PF00089 | 322.84 | 171 | 881 |
| HOGDR01 | 947085 | 847 | blastx.2 HMMER 1.8 | (AC003965) SP001LA [Homo sapiens] | gb AAB93671.1 PF00089 | 99% | 165 | 890 |
| HOGDR01 | 947085 | 847 | blastx.2 HMMER 1.8 | (AC003965) SP001LA [Homo sapiens] | gb AAB93671.1 PF00089 | 320.16 | 161 | 871 |
| HOGDR01 | 947085 | 847 | blastx.2 HMMER 1.8 | (AC003965) SP001LA [Homo sapiens] | gb AAB93671.1 PF00089 | 99% | 155 | 967 |
| HOGDR01 | 947085 | 847 | blastx.2 HMMER 1.8 | (AC003965) SP001LA [Homo sapiens] | gb AAB93671.1 PF00089 | 82.96 | 729 | 361 |
| HOGDR01 | 947085 | 847 | blastx.2 HMMER 1.8 | (AC003965) SP001LA [Homo sapiens] | gb AAB93671.1 PF00089 | 100% | 735 | 340 |
| HOGDR01 | 947085 | 847 | blastx.2 HMMER 1.8 | (AC003965) SP001LA [Homo sapiens] | gb AAB93671.1 PF00089 | 94% | 36 | 743 |
| HOGDR01 | 947085 | 847 | blastx.2 HMMER 1.8 | (AC003965) SP001LA [Homo sapiens] | gb AAB93671.1 PF00089 | 309.92 | 56 | 724 |
| HOGDR01 | 947085 | 847 | blastx.2 HMMER 1.8 | (AC003965) SP001LA [Homo sapiens] | gb AAB93671.1 PF00089 | 93% | 35 | 742 |
| HOGDR01 | 947085 | 847 | blastx.2 HMMER 1.8 | (AC003965) SP001LA [Homo sapiens] | gb AAB93671.1 PF00089 | 397.1 | 10 | 642 |
| HOGDR01 | 947085 | 847 | blastx.2 HMMER 1.8 | (AC003965) SP001LA [Homo sapiens] | gb AAB93671.1 PF00089 | 98% | 4 | 642 |
| HOGDR01 | 947085 | 847 | blastx.2 HMMER 1.8 | (AC003965) SP001LA [Homo sapiens] | gb AAB93671.1 PF00089 | 420.7 | 250 | 1026 |

| | | | | | | | | | |
|---------|--------|-----|-------------|--|----------------------|-------------------|--|-----------------|-------------------|
| | | | 2.1.1 | beta-lactamase (EC 3.5.2.6) - phage phi-X174 | pir S47061 S47061 | 95% | | | |
| | | | blastx.2 | | | | | 169 | 1026 |
| HHEKZ12 | 878267 | 316 | HMMER 1.8 | PFAM: Beta-lactamases | PF00144 | 132.1 | | 102 | 380 |
| | | | blastx.2 | beta-lactamase (EC 3.5.2.6) - phage phi-X174 | pir S47061 S47061 | 98% 65% | | 21 377 | 377 436 |
| HHELA35 | 878217 | 317 | HMMER 2.1.1 | PFAM: Beta-lactamase | PF00144 | 175.4 | | 118 | 450 |
| | | | blastx.2 | beta-lactamase (EC 3.5.2.6) - phage phi-X174 | pir S47061 S47061 | 98% | | 37 | 450 |
| HSYBQ34 | 972295 | 849 | HMMER 1.8 | PFAM: Beta-lactamases | PF00144 | 387.58 | | 2697 | 3473 |
| HFCBA44 | 948533 | 319 | HMMER 1.8 | PFAM: Carboxylesterases | PF00135 | 34.24 | | 315 | 485 |
| | | | blastx.2 | thiolesterase B (EC 3.---) precursor - mallard | pir A47162 A47162 | 56% 60% 48% | | 2 423 184 | 208 482 264 |
| HOUBE50 | 948519 | 320 | HMMER 1.8 | PFAM: Carboxylesterases | PF00135 | 55.97 | | 16 | 243 |
| | | | blastx.2 | Neurologin 3 isoform HNL3s (Fragment). | sp AAF71231 AAF71231 | 70% | | 31 | 243 |
| HDPAS16 | 734057 | 321 | HMMER 2.1.1 | PFAM: Carbamoyl-phosphate synthase (CPSase) | PF00289 | 137.8 | | 220 | 495 |
| | | | blastx.2 | 3-methylcrotonyl-CoA carboxylase biotin-containing 1 | sp BAA99407 BAA99407 | 89% | | 112 | 495 |
| HFLAA23 | 960332 | 322 | HMMER 2.1.1 | PFAM: FGYY family of carbohydrate kinases | PF00370 | 314 | | 137 | 784 |

| | | | | | | | | | |
|---------|---------|-----|-------------|--|---|-------------------|--------------------------|--------------------------|--------------------------|
| | | | | blastx.2 | L-xylulokinase (EC 2.7.1.53) - Escherichia coli | pir[S47801]S47801 | 86% | 8 | 784 |
| HCFMZ90 | 922112 | 323 | HMMER 1.8 | PFAM: Beta-ketoacyl synthases | PF00109 | | 194.57 | 291 | 872 |
| | | | blastx.2 | CDNA FLJ20604 FIS, CLONE KAT06449. | sp BAA91286 BAA91286 | | 92% 98% 59% | 255 67 5 | 866 300 100 |
| HFCE27 | 1103330 | 324 | blastx.2 | CDNA FLJ20604 FIS, CLONE KAT06449. | sp BAA91286 BAA91286 | | 94% 86% | 506 198 | 1120 491 |
| HFCE27 | 922115 | 850 | HMMER 2.1.1 | PFAM: Beta-ketoacyl synthase | PF00109 | | 206.2 | 372 | 1001 |
| | | | blastx.14 | (AE000752) 3-oxoacyl-[acyl-carrier-protein] synthase II [Aquifex aeolicus] | gi 2984031 gb AAC07574.1 | | 53% 78% 75% 37% | 393 195 939 250 | 920 251 986 297 |
| HSDFK78 | 1155464 | 325 | blastx.2 | biotin sulfoxide reductase (EC 1.-.-.-) 2 - Escherichia coli | pir H64949 H64949 | | 89% | 1 | 306 |
| HSDFK78 | 582754 | 851 | HMMER 2.1.1 | PFAM: Prokaryotic molybdopterin oxidoreductases | PF00384 | | 34.8 | 297 | 374 |
| HSDJX58 | 891067 | 326 | HMMER 1.8 | PFAM: NADH-Ubiquinone/plastoquinone, various chains | PF00361 | | 97.09 | 1128 | 1487 |
| | | | blastx.2 | hypothetical protein b2484 - Escherichia coli (strain K-12) | pir C65024 C65024 | | 82% | 735 | 1487 |
| HSDJX58 | 956591 | 852 | HMMER 1.8 | PFAM: NADH-Ubiquinone/plastoquinone | PF00361 | | 100.08 | 387 | 19 |

| | | | | , various chains | | | | |
|---------|---------|-----|-------------|---|---------------------------|--------------------------|--------------------------|------------------------|
| | | | blastx.2 | NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 [Escherichia coli] | dbj BAA16372.1 | 100% | 814 | 1572 |
| HSLHV27 | 1105339 | 327 | blastx.2 | NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain L - Escherichia coli | pir D64999 D64999 | 93% | 94 | 927 |
| HSLHV27 | 964075 | 853 | HMMER 2.1.1 | PFAM: NADH-Ubiquinone/plastoquinone (complex I), various chains | PF00361 | 115.1 | 917 | 615 |
| | | | blastx.2 | NADH dehydrogenase I, submit nuol [Escherichia coli] | emb CAA48371.1 | 99% | 91 | 954 |
| HNGFU12 | 1128272 | 328 | blastx.2 | REVERSE TRANSCRIPTASE (476 AA) (FRAGMENT). | sp Q85732 Q85732 | 55% | 109 | 543 |
| HNGFU12 | 971170 | 854 | HMMER 1.8 | PFAM: RNase H | PF00075 | 55.68 | 102 | 290 |
| | | | blastx.14 | reverse transcriptase (476 AA) [Woolly monkey sarcoma virus] | gj J930259 emb CAA33367.1 | 44% 60% | 96 1 | 422 75 |
| HWLKA89 | 1105515 | 329 | blastx.2 | POL.PROTEIN. | sp Q9WIK9 Q9WIK9 | 51% 54% 55% 64% | 560 885 135 448 | 186 577 1 398 |
| HWLKA89 | 735158 | 855 | HMMER 1.8 | PFAM: RNase H | PF00075 | 47.76 | 25 | 165 |
| HLWRU48 | 1162653 | 330 | blastx.2 | ENDOGENOUS | sp O15803 O15803 | 84% | 739 | 984 |

[illegible]

| | | | | | | | | |
|---------|---------|-----|-------------|--|----------------------|---------------------------------|--------------------------------|---------------------------------|
| HMACX92 | 1151497 | 334 | blastx.2 | (SODM) L-serine dehydratase (EC 4.2.1.13) - rat | pir S01009 DWRRTT | 50% | 176 | 1132 |
| HMACX92 | 922250 | 860 | HMMER 2.1.1 | PFAM: Pyridoxal-phosphate dependent enzyme | PF00291 | 224.5 | 203 | 1105 |
| | | | blastx.2 | serine dehydratase (AA 1 - 327) [Rattus norvegicus] | emb CAA68721.1 | 61% | 197 | 1153 |
| HNTBW57 | 1193070 | 335 | blastx.2 | CDNA FLJ10916 FIS, CLONE OVARC1000309, WEAKLY SIMILAR TO 1 | sp BAA91904 BAA91904 | 80% 100% | 958 613 | 1302 777 |
| HNTBW57 | 867327 | 861 | HMMER 1.8 | PFAM: Serine/threonine dehydratases, cysteine synthase and cystathionine | PF00291 | 41.43 | 425 | 673 |
| HBSDC13 | 1105677 | 336 | blastx.2 | tartronate-semialdehyde synthase (EC 4.1.1.47) - Escherichia coli | pir JT0742 JT0742 | 68% 83% 51% 85% 96% | 353 124 622 840 47 | 718 423 990 959 130 |
| HBSDC13 | 657402 | 862 | HMMER 1.8 | PFAM: Thiamine pyrophosphate enzymes | PF00205 | 26.75 | 3 | 182 |
| HCWBX21 | 920486 | 337 | HMMER 1.8 | PFAM: Thiamine pyrophosphate enzymes | PF00205 | 22.15 | 82 | 261 |
| | | | blastx.2 | tartronate-semialdehyde synthase (EC 4.1.1.47) - Escherichia coli | pir JT0742 JT0742 | 88% 96% 43% | 85 8 374 | 369 91 442 |
| HFRBW72 | 916944 | 338 | HMMER 2.1.1 | PFAM: Thiamine pyrophosphate enzymes | PF00205 | 92.9 | 443 | 664 |

| | | | | | | | | |
|---------|---------|-----|----------------|---|-------------------------------|-------------------|-------------------|-------------------|
| | | | blastx.2 | pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2) - Escherichia coli | pir A23648 DEECPC | 81% | 407 | 676 |
| HSLJX23 | 1105530 | 339 | blastx.2 | tartarate-semialdehyde synthase (EC 4.1.1.47) - Escherichia coli | pir JT0742 JT0742 | 98% | 2 | 496 |
| HSLJX23 | 837470 | 863 | HMMER 1.8 | PFAM: Thiamine pyrophosphate enzymes | PF00205 | 57.57 | 2 | 193 |
| HSLJX90 | 1105297 | 340 | blastx.2 | pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2) - Escherichia coli | pir A23648 DEECPC | 100% | 1 | 438 |
| HSLJX90 | 787575 | 864 | HMMER 2.1.1 | PFAM: Thiamine pyrophosphate enzymes | PF00205 | 95.2 | 2 | 274 |
| HAUAI67 | 1102604 | 341 | blastx.2 | HSPC150. | sp AAF29114 AAF29 114 | 100% | 137 | 727 |
| HAUAI67 | 929241 | 865 | HMMER 1.8 | PFAM: Ubiquitin- conjugating enzymes | PF00179 | 128.71 | 236 | 508 |
| | | | blastx.14 | ubiquitin-conjugating enzyme [Schizosaccharomyces pombe] | gi 2330662 emb CAB 11183.1 | 54% 67% 32% | 344 242 132 | 514 334 224 |
| HDPTA89 | 953718 | 342 | HMMER 1.8 | PFAM: Ubiquitin- conjugating enzymes | PF00179 | 74.19 | 173 | 424 |
| | | | blastx.2 | UBC6P HOMOLOG. | sp Q9QX58 Q9QX58 | 95% | 173 | 430 |
| HMCBN45 | 927125 | 343 | HMMER 1.8 | PFAM: Ubiquitin- conjugating enzymes | PF00179 | 115.78 | 234 | 677 |
| | | | blastx.2 | hypothetical protein R09B3.4 - Caenorhabditis elegans | pir T24069 T24069 | 53% | 216 | 680 |
| HTTJY18 | 1223495 | 344 | blastx.2 | Non-Canonical Ubiquitin | sp CAB83212 CAB8 | 83% | 376 | 1281 |

| | | | | | Conjugating Enzyme 1 (NCUBE1). | 3212 | 100% | 330 | 365 |
|---------|---------|-----|----------------|--|---|---|--------------|------------|-------------|
| HTTJY18 | 950989 | 866 | HMMER 1.8 | | PFAM: Ubiquitin- conjugating enzymes (AF151834) CGI-76 protein [Homo sapiens] | PF00179 | 73.94 | 334 | 657 |
| HMAJL09 | 1157337 | 345 | blastx.2 | | hypothetical 29.7K protein, ibpA-gyrB intergenic region - Escherichia coli (strain K- 12) | gb AAD34071.1 AF1 51834.1 pir B65172 QQECGB | 99% 98% | 292 269 | 1263 526 |
| HMAJL09 | 950168 | 867 | HMMER 1.8 | | PFAM: ADP-glucose pyrophosphorylase | PF00483 | 150.92 | 20 | 256 |
| HSVCH37 | 558195 | 346 | blastx.14 | | f270 [Escherichia coli] | gi 290545 gb AAA62 048.1 | 100% 100% | 254 468 | 469 512 |
| HTOCG37 | 708888 | 347 | HMMER 2.1.1 | | PFAM: 3'5'-cyclic nucleotide phosphodiesterase | PF00233 | 30 | 18 | 98 |
| HBXAW47 | 771624 | 348 | HMMER 2.1.1 | | PFAM: 3'5'-cyclic nucleotide phosphodiesterase | PF00233 | 65.1 | 42 | 215 |
| HBXAW27 | 909801 | 349 | blastx.2 | | 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 8B, 1 | pir JE0293 JE0293 | 100% 53% | 6 179 | 203 340 |
| | | | HMMER 2.1.1 | | PFAM: Protein phosphatase 2C | PF00481 | 80.5 | 273 | 560 |
| | | | blastx.2 | | PROTEIN PHOSPHATASE 2C | sp Q9Z1Z6 Q9Z1Z6 | 85% | 270 | 578 |
| | | | HMMER 2.1.1 | | PFAM: Phosphatidylinositol- | PF00388 | 113.6 | 1642 | 1797 |

| | | | | specific phospholipase C, X domain | | | | | |
|---------|--------|-----|----------------|--|--------------------------|---|--|---|--|
| | | | blastx.2 | Phospholipase C-beta-1a. | sp CAB98142 CAB9 8142 | 97% | 1243 | 1803 | |
| HSLJE54 | 926924 | 350 | HMMER 2.1.1 | PFAM: Pyridoxal- dependent decarboxylase conserved domain | PF00282 | 35.8 | 342 | 536 | |
| | | | blastx.2 | CYSTEINE SULFINIC ACID DECARBOXYLASE- RELATED PROTEIN 4. | sp Q9UNJ5 Q9UNJ5 | 98% 92% 85% 100% | 198 542 721 885 | 548 739 885 908 | |
| HBXBG65 | 932780 | 351 | HMMER 1.8 | PFAM: Cytochrome P450 | PF00067 | 46.55 | 2 | 535 | |
| | | | blastx.2 | CHOLESTEROL 24- HYDROXYLASE. | sp Q9Y6A2 Q9Y6A2 | 98% | 2 | 535 | |
| HE8CG83 | 933609 | 352 | HMMER 2.1.1 | PFAM: Protein phosphatase 2C | PF00481 | 42.6 | 757 | 942 | |
| | | | blastx.2 | SCOP. | sp Q9WTR8 Q9WTR 8 | 90% 70% 70% 60% 43% 30% 36% | 321 712 1 977 41 118 369 | 707 1110 348 1021 151 279 443 | |
| HOGCW55 | 953161 | 353 | HMMER 2.1.1 | PFAM: Aminotransferases class- V | PF00266 | 56.5 | 132 | 341 | |
| | | | blastx.2 | probable phosphoserine transaminase (EC 2.6.1.52), progesterone- | pir A26998 A26998 | 85% 77% | 132 355 | 356 381 | |

| | | | | | | | | |
|---------|--------|-----|----------------------------|---|-------------------------------------|-------------------------|----------------------|--------------------------|
| HNTND64 | 954871 | 354 | HMMER 2.1.1 blastx.2 | induced, endometrial - rabbit PFAM: Cytochrome P450 | PF00067 | 28.2 | 10 | 225 |
| | | | | cytochrome P450 - golden hamster | pir 48164 48164 | 37% 47% | 10 261 | 264 329 |
| HHAWC08 | 957942 | 355 | HMMER 1.8 | PFAM: IMP dehydrogenase / GMP reductase | PF00478 | 231.99 | 361 | 978 |
| | | | blastx.2 | Guanosine monophosphate reductase isolog. | sp BAA93080 BAA9 3080 | 100% 100% | 334 975 | 975 1376 |
| HFPEN04 | 964824 | 356 | HMMER 1.8 | PFAM: Aminotransferases class- III pyridoxal-phosphate | PF00202 | 33.54 | 259 | 489 |
| | | | blastx.2 | CG8745 PROTEIN. | sp Q9VU95 Q9VU95 | 62% | 148 | 492 |
| HTZMB51 | 496523 | 357 | HMMER 2.1.1 blastx.2 | PFAM: Lyase adenylosuccinate lyase (EC 4.3.2.2) - Escherichia coli | PF00206 pir S19212 S19212 | 112.9 97% 71% | 61 73 2 | 399 399 127 |
| HNHDK43 | 529500 | 358 | HMMER 1.8 blastx.2 | PFAM: tRNA synthetases class II lysine--tRNA ligase (EC 6.1.1.6) - Escherichia coli | PF00152 pir B65073 SYECKT | 55.51 85% 90% | 208 58 368 | 372 372 397 |
| HTTDP32 | 558751 | 359 | HMMER 2.1.1 blastx.2 | PFAM: tRNA synthetases class I (L, M and V) PROBABLE LEUCYL- TRNA SYNTHETASE, MITOCHONDRIAL | PF00133 sp Q15031 SYLM_H UMAN | 76 98% 84% 45% | 7 1 267 320 | 261 261 365 424 |

| | | | | | | | | |
|----------|--------|-----|----------------------------|--|------------------------------|----------------------|-------------------|-------------------|
| HSLEP27 | 572920 | 360 | HMMER 2.1.1 blastx.2 | PRECURSOR 1 PFAM: tRNA synthetases class I (I, L, M and V) leucine-tRNA ligase (EC 6.1.1.4) [validated] - Escherichia coli | PF00133 pir H64798 SYECL | 133.5 96% 96% | 5 14 405 | 409 599 |
| HMTAL73 | 621705 | 361 | HMMER 2.1.1 blastx.2 | PFAM: Isocitrate and isopropylmalate dehydrogenases isocitrate dehydrogenase (NAD+) (EC 1.1.1.41) beta chain isoform B - human | PF00180 pir T13147 T13147 | 94.5 75% 100% | 241 103 2 | 423 450 100 |
| HMHQBQ53 | 715301 | 362 | HMMER 2.1.1 blastx.2 | PFAM: Nucleotidyl transferase GDP-MANNOSE PYROPHOSPHORYLAS E.A. | PF00483 sp Q9Y5P5 Q9Y5P5 | 45.8 100% 100% | 237 231 376 | 368 377 423 |
| HBICG44 | 715860 | 363 | HMMER 2.1.1 blastx.2 | PFAM: Thiolase 3-oxoacyl-CoA thiolase - human | PF00108 pir S43440 S43440 | 33.1 100% | 189 189 | 272 272 |
| HSKXN70 | 753717 | 364 | HMMER 2.1.1 blastx.2 | PFAM: TPR Domain CG5038 PROTEIN. | PF00515 sp Q9VF81 Q9VF81 | 31.4 40% | 267 114 | 347 344 |
| HPIAC32 | 815942 | 365 | HMMER 2.1.1 blastx.2 | PFAM: Histidine acid phosphatase acid phosphatase (EC 3.1.3.2) precursor - Escherichia coli | PF00328 pir B36733 B36733 | 118.4 77% 92% | 75 3 341 | 338 518 463 |

| | | | | | | | | |
|---------|--------|-----|----------------------------|--|--|---------------------|-----------------|-------------------|
| HHPFP57 | 835955 | 366 | HMMER 2.1.1 blastx.2 | PFAM: Signal peptidase I | PF00461 | 32.1 | 218 | 514 |
| HFKJW01 | 836491 | 367 | HMMER 2.1.1 blastx.2 | CG11110 PROTEIN. PFAM: Aldehyde dehydrogenase family lactaldehyde dehydrogenase (EC 1.2.1.22) aldA - Escherichia coli | sp Q9V959 Q9V959 PF00171 pir A38165 A38165 | 57% 174 100% | 140 96 96 | 574 440 440 |
| HSDFL63 | 836498 | 368 | HMMER 2.1.1 blastx.2 | PFAM: Aldehyde dehydrogenase family RETINALDEHYDE- SPECIFIC DEHYDROGENASE TYPE 2 (EC 1.2.1.-) (RALDH(II)) (RALDH- 2). | PF00171 sp O94788 DHAS_H UMAN | 127.4 100% | 1 1 | 234 249 |
| HLDOO08 | 857070 | 369 | HMMER 2.1.1 blastx.2 | PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 CDNA FLJ10785 FIS, CLONE NT2RP4000457, WEAKLY SIMILAR TO 1 | PF00443 sp BAA91807 BAA9 1807 | 32.4 100% 80% | 36 3 403 | 137 401 570 |
| HMSHN43 | 867363 | 370 | HMMER 2.1.1 blastx.2 | PFAM: Nucleotidyl transferase GDP-MANNOSE PYROPHOSPHORYLAS E A. | PF00483 sp Q9Y5P5 Q9Y5P5 | 53.7 90% | 70 64 | 231 342 |
| HBXCT92 | 871044 | 371 | HMMER | PFAM: Nucleotidyl | PF00483 | 49.7 | 105 | 473 |

| | | | | | | | | | |
|---------|--------|-----|--|---------------|--|-----------------------|----------------------------|------------------------------|-----------------------------|
| | | | | transferase | | | | | |
| | | | | blastx.2 | Eukaryotic translation initiation factor EIF2B subunit 3. | sp AAAF91351 AAF91351 | 97% | 96 | 1451 |
| H6EDP44 | 875744 | 372 | | HMME 2.1.1 | PFAM: Nucleotidyl transferase | PF00483 | 129.6 | 190 | 768 |
| | | | | blastx.2 | GDP-MANNOSE PYROPHOSPHORYLAS E B. | sp Q9Y5P6 Q9Y5P6 | 99% 100% 100% 32% | 199 804 65 837 | 801 968 187 938 |
| HLJBF94 | 875745 | 373 | | HMME 2.1.1 | PFAM: Nucleotidyl transferase | PF00483 | 89.2 | 261 | 539 |
| | | | | blastx.2 | GDP-MANNOSE PYROPHOSPHORYLAS E B. | sp Q9Y5P6 Q9Y5P6 | 81% | 258 | 668 |
| HTEHO28 | 877182 | 374 | | HMME 1.8 | PFAM: Pyridine nucleotide-disulphide oxidoreductases class-I | PF00070 | 206.97 | 1166 | 441 |
| | | | | blastx.2 | Thioredoxin reductase TR2 (Fragment). | sp AAD51325 AAD51325 | 97% 85% 97% 41% | 1226 1857 2123 1383 | 432 1147 1869 1315 |
| HE9PC30 | 880696 | 375 | | HMME 1.8 | PFAM: Ubiquitin-conjugating enzymes CGI-76 PROTEIN. | PF00179 | 69.1 | 85 | 285 |
| | | | | blastx.2 | | sp Q9Y385 Q9Y385 | 98% 96% 60% | 43 555 527 | 381 638 586 |
| HLMDN29 | 881288 | 376 | | HMME 2.1.1 | PFAM: Ubiquitin carboxyl-terminal hydrolase family 2 | PF00443 | 34.2 | 315 | 506 |

| | | | | | | | | |
|---------|--------|-----|----------------|--|----------------------|-------|-----|------|
| | | | blastx.2 | CG8830 PROTEIN. | sp Q9V6C0 Q9V6C0 | 43% | 9 | 218 |
| HWBCF78 | 911355 | 377 | HMMER 2.1.1 | PFAM: Myosin head (motor domain) | PF00063 | 31% | 399 | 503 |
| | | | blastx.2 | myosin-1f - mouse | pir A59300 A59300 | 89% | 148 | 288 |
| HUKEN49 | 911465 | 378 | HMMER 1.8 | PFAM: Myosin head (motor domain) (contains ATP/GTP binding P-loop) | PF00063 | 53.97 | 125 | 274 |
| | | | blastx.2 | Myosin V. | sp AAF78910 AAF78910 | 66% | 3 | 128 |
| | | | | | | 54% | 125 | 274 |
| | | | | | | 40% | 333 | 431 |
| HCUDS02 | 914401 | 379 | HMMER 2.1.1 | PFAM: Nucleotidyl transferase | PF00483 | 91.6 | 84 | 650 |
| | | | blastx.2 | CDNA FLJ10137 FIS, CLONE HEMBA1003136, WEAKLY SIMILAR TO 1 | sp BAA91460 BAA91460 | 98% | 78 | 782 |
| | | | | | | 99% | 907 | 1335 |
| | | | | | | 64% | 755 | 1006 |
| HTTJU40 | 914402 | 380 | HMMER 2.1.1 | PFAM: Nucleotidyl transferase | PF00483 | 23.8 | 43 | 372 |
| | | | blastx.2 | GDP-MANNULOSE PYROPHOSPHORYLAS E A. | sp Q9Y5P5 Q9Y5P5 | 100% | 40 | 417 |
| | | | | | | 100% | 440 | 496 |
| HFXJX41 | 915649 | 381 | HMMER 2.1.1 | PFAM: Phosphoglucosyltransferase/phosphomannomutase | PF00408 | 36.5 | 491 | 682 |
| | | | blastx.2 | hypothetical protein b0644 - Escherichia coli | pir B64799 B64799 | 100% | 3 | 308 |
| | | | | | | 100% | 308 | 496 |
| | | | | | | 45% | 6 | 308 |
| | | | | | | 43% | 3 | 308 |

| | | | | | | | | | |
|---------|--------|-----|----------------|--|----------------------|--|-------|-----|-----|
| HSLCK91 | 915650 | 382 | HMMER 2.1.1 | PFAM: Phosphoglucosyltransferase/phosphomannomutase | | | 36% | 6 | 308 |
| | | | blastx.2 | phosphoglucosyltransferase (EC 5.4.2.2) - Escherichia coli | pir G64803 G64803 | | 84% | 1 | 375 |
| HSLAO29 | 917349 | 383 | HMMER 2.1.1 | PFAM: Serine hydroxymethyltransferase | PF00464 | | 43 | 363 | 431 |
| | | | blastx.2 | SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR 1 1 | sp P34897 GLYM_HUMAN | | 92% | 137 | 373 |
| | | | | | | | 52% | 363 | 536 |
| | | | | | | | 48% | 427 | 534 |
| HRDBJ38 | 917583 | 384 | HMMER 2.1.1 | PFAM: Trypsin | PF00089 | | 48.9 | 20 | 523 |
| | | | blastx.2 | SERINE PROTEASE (FRAGMENT). | sp O97658 O97658 | | 62% | 23 | 856 |
| HOUES64 | 918119 | 385 | HMMER 2.1.1 | PFAM: Aldehyde dehydrogenase family | PF00171 | | 138.5 | 3 | 278 |
| | | | blastx.2 | lactaldehyde dehydrogenase (EC 1.2.1.22) aldA - Escherichia coli | pir A38165 A38165 | | 98% | 3 | 275 |

| | | | | | | | | |
|---------|--------|-----|----------------------------|---|--|----------------------------------|-------------------------------|---------------------------------|
| HWLHU02 | 918520 | 386 | HMMER 2.1.1 blastx.2 | PFAM: Hexokinase Hexokinase II. | PF00349 | 286.7 | 3 | 395 |
| HEAHA84 | 919363 | 387 | HMMER 2.1.1 blastx.2 | PFAM: Myosin head (motor domain) myosin I myr 4 - rat | sp CAA86476 CAA86476 PF00063 pir A53933 A53933 | 79% 66% 36.3 | 3 3 87 | 395 395 245 |
| HBMXQ90 | 922114 | 388 | HMMER 2.1.1 blastx.2 | PFAM: Beta-ketoacyl synthase CDNA FLJ20604 FIS, CLONE KAT06449. | PF00109 sp BAA91286 BAA91286 PF00334 | 20.5 66% 96% 103.55 | 218 301 215 362 | 301 462 301 757 |
| HOEJV72 | 930778 | 389 | HMMER 1.8 blastx.2 | PFAM: Nucleoside diphosphate kinases NM23-H7. | sp Q9Y5B8 Q9Y5B8 | 95% 29% 175.49 | 89 368 536 | 847 754 1558 |
| HRDBH58 | 933364 | 390 | HMMER 1.8 blastx.2 | PFAM: Aldehyde dehydrogenases probable aldehyde dehydrogenase PA4073 [imported] - Pseudomonas aeruginosa (strain PAO1) | PF00171 pir H83136 H83136 | 29% 34% | 569 244 | 1528 450 |
| HCE3E13 | 951413 | 391 | HMMER 2.1.1 blastx.2 | PFAM: tRNA synthetases class I (L, M and V) valine-tRNA ligase precursor, mitochondrial - fission yeast (Schizosaccharomyces pombe) | PF00133 pir T39630 T39630 | 95.6 40% 41% 44% 83% | 148 151 4 569 645 | 603 603 213 649 662 |
| HUKFO68 | 951652 | 392 | HMMER | PFAM: Hexokinase | PF00349 | 173.1 | 83 | 340 |

| | | | | | | | | |
|---------|--------|-----|-------------|--|----------------------|-------|-----|-----|
| | | | 2.1.1 | Hexokinase I (Fragment). | sp AAF28854 AAF28854 | 76% | 83 | 355 |
| | | | blastx.2 | | | 47% | 83 | 373 |
| | | | | | | 80% | 3 | 80 |
| | | | | | | 36% | 3 | 77 |
| HFXJW08 | 959204 | 393 | HMMER 2.1.1 | PFAM: tRNA synthetases class I (I, L, M and V) | PF00133 | 86.6 | 224 | 487 |
| | | | blastx.2 | leucine--tRNA ligase (EC 6.1.1.4) [validated] - Escherichia coli | pir H64798 SYECL | 82% | 224 | 676 |
| | | | | | | 100% | 3 | 230 |
| HBTAD04 | 407351 | 394 | blastx.2 | malate synthase (EC 4.1.3.2) A - Escherichia coli | pir A32649 SYECM A | 98% | 240 | 1 |
| HBTAD04 | 422687 | 868 | HMMER 2.1.1 | PFAM: Acetyltransferase (GNAT) family | PF00583 | 36.5 | 427 | 161 |
| HE8FG51 | 465267 | 395 | HMMER 2.1.1 | PFAM: Eukaryotic initiation factor 5A hypusine (eIF-5A) | PF01287 | 165.7 | 4 | 258 |
| | | | blastx.2 | EIF-5A2. | sp AAF98810 AAF98810 | 98% | 7 | 267 |
| HTPDU31 | 503077 | 396 | HMMER 2.1.1 | PFAM: haloacid dehalogenase-like hydrolase | PF00702 | 26.3 | 147 | 296 |
| | | | blastx.2 | DJ37E16.5 (NOVEL PROTEIN SIMILAR TO NITROPHENYLPHOSP HATASES 1 | sp Q9UGY2 Q9UGY2 | 94% | 54 | 323 |
| | | | | | | 100% | 25 | 72 |
| | | | | | | 100% | 323 | 364 |
| HMUBV12 | 549423 | 397 | HMMER 2.1.1 | PFAM: Hyaluronidase | PF01630 | 50.7 | 196 | 303 |
| HMHBS90 | 574062 | 398 | HMMER | PFAM: UBA domain | PF00627 | 35.6 | 436 | 543 |

| | | | | | | | | | |
|---------|--------|-----|----------------------------|--|---|-------------------------------------|----------------------------|-------------------------|--------------------------|
| | | | 2.1.1 blastx.2 | | HRHFB2157-LIKE PROTEIN (FRAGMENT). | sp Q9UHX4 Q9UHX 4 | 61% 100% | 58 3 | 561 59 |
| HLHGH34 | 575733 | 399 | HMMER 1.8 blastx.2 | | PFAM: C-5 cytosine- specific DNA methylases PUTATIVE DNA CYTOSINE METHYLTRANSFERAS E DNMT2. | PF00145 sp O43669 O43669 | 33.72 100% | 284 2 | 436 436 |
| HELHC55 | 577384 | 400 | HMMER 2.1.1 blastx.2 | | PFAM: Copper amine oxidase amine oxidase (copper- containing) (EC 1.4.3.6) tynA precursor - Escherichia coli | PF01179 pir E64889 E64889 | 88.8 96% | 39 3 | 173 173 |
| HKAAZ66 | 592105 | 401 | HMMER 2.1.1 blastx.2 | | PFAM: Calpain family cysteine protease Calpain large polypeptide L2. | PF00648 sp AAF99682 AAF99 682 | 164.9 99% 98% 87% | 222 90 416 648 | 422 422 640 671 |
| HHSCN33 | 657367 | 402 | HMMER 2.1.1 blastx.2 | | PFAM: HECT-domain (ubiquitin-transferase). NEDD4-like ubiquitin ligase 1. | PF00632 sp BAB13352 BAB1 3352 | 58.3 91% | 166 1 | 348 390 |
| HNGJQ15 | 660310 | 403 | HMMER 2.1.1 blastx.2 | | PFAM: Histone deacetylase family CDNA FLJ10170 FIS, CLONE HEMBA1003690. | PF00850 sp BAA91474 BAA9 1474 | 33.2 75% 47% | 70 70 196 | 192 192 264 |

| | | | | | | | | |
|---------|--------|-----|----------------------------|--|-------------------------------------|---|---|---|
| HDJME16 | 661396 | 404 | HMMER 2.1.1 blastx.2 | WEAKLY SIMILAR TO 1 PFAM: FF domain | PF01846 | 53.7 | 34 | 183 |
| HNTNR64 | 670033 | 405 | HMMER 2.1.1 blastx.2 | HUNTINGTON YEAST PARTNER C. PFAM: Kelch motif | sp Q9WVC9 Q9WV C9 PF01344 | 84% | 1 | 486 |
| HMICO24 | 677036 | 406 | HMMER 2.1.1 blastx.2 | CDNA FLJ11078 FIS, CLONE PLACE1005102, WEAKLY SIMILAR TO 1 PFAM: Kelch motif | sp BAA91990 BAA9 1990 PF01344 | 36% 34% 47% 43% 89.1 | 30 54 347 350 25 | 344 314 448 445 147 |
| HSIAC23 | 679292 | 407 | HMMER 2.1.1 blastx.2 | LYMPHOCYTE ACTIVATION- ASSOCIATED PROTEIN. PFAM: Chlorohydrolase | sp Q9Y2X2 Q9Y2X2 PF01685 | 92% 49% 55% 44% 52% 80% 100% 100% 47% | 25 25 55 25 85 285 242 2 236 194 | 261 243 231 243 234 344 283 22 286 358 |
| HSLFL74 | 685897 | 408 | HMMER 2.1.1 | GUANINE DEAMINASE (EC 3.5.4.3) (GUANASE) (GUANINE 1) PFAM: RNB-like proteins | sp Q9RI11 GUAD_ MOUSE PF00773 | 62% 87% 243.4 | 62 10 21 | 457 108 425 |

| | | | | | | | | |
|---------|--------|-----|-------------|--|----------------------|-------|-----|------|
| | | | blastx.2 | exoribonuclease II (EC 3.1.13.1) - Escherichia coli | pir A64877 A64877 | 78% | 705 | 1346 |
| | | | | | | 97% | 3 | 428 |
| | | | | | | 75% | 434 | 892 |
| | | | | | | 94% | 877 | 933 |
| | | | | | | 48% | 990 | 1064 |
| HSDJD53 | 698259 | 409 | HMMER 2.1.1 | PFAM: Nitroreductase family | PF00881 | 86.9 | 193 | 513 |
| | | | blastx.2 | hypothetical protein, 20K (selD-sppA intergenic region) - Escherichia coli | pir A40360 A40360 | 80% | 190 | 624 |
| HCEBF33 | 702955 | 410 | HMMER 2.1.1 | PFAM: HECT-domain (ubiquitin-transferase). | PF00632 | 248.4 | 15 | 581 |
| | | | blastx.2 | Ubiquitin-protein ligase 1. | sp AAF36454 AAF36454 | 51% | 21 | 581 |
| HAPQW27 | 705518 | 411 | HMMER 2.1.1 | PFAM: Sterol O-acyltransferase | PF01800 | 180.1 | 1 | 279 |
| | | | blastx.2 | AGRP1 PROTEIN. | sp O75907 O75907 | 62% | 1 | 432 |
| HCFLZ28 | 707183 | 412 | HMMER 2.1.1 | PFAM: ThiF family | PF00899 | 93.7 | 166 | 444 |
| | | | blastx.2 | SUMO-1-ACTIVATING ENZYME E1 N SUBUNIT. | sp O95717 O95717 | 95% | 142 | 447 |
| | | | | | | 83% | 495 | 545 |
| HWCAB58 | 710377 | 413 | HMMER 2.1.1 | PFAM: Kelch motif | PF01344 | 53.3 | 21 | 164 |
| | | | blastx.2 | Kelch related protein 1. | sp CAC08185 CAC08185 | 49% | 3 | 275 |
| | | | | | | 59% | 302 | 448 |
| | | | | | | 29% | 3 | 266 |
| | | | | | | 28% | 18 | 245 |
| HLMMC57 | 713770 | 414 | HMMER 2.1.1 | PFAM: Acetyltransferase (GNAT) family | PF00583 | 31 | 272 | 406 |

| | | | | | | | | |
|---------|--------|-----|--|---|---|---|--|--|
| HMELH37 | 717556 | 415 | blastx.2 HMMER 2.1.1 blastx.2 | diamine N- acetyltransferase (EC 2.3.1.57) - spiny mouse (Mus saxicola) PFAM: Initiation factor 2 subunit family probable translation initiation factor eIF-2B delta chain - human (fragment) PFAM: MaoC like domain membrane protein maoC - Escherichia coli PFAM: MaoC like domain | pir S43430 S43430 PF01008 pir T08757 T08757 PF01575 PF01575 PF00583 pir S43430 S43430 PF00899 sp Q9VYY3 Q9VYY 3 PF01613 sp P75893 P75893 | 39% 55% 101.1 95% 96% 117.2 100% 117.2 24.9 40% 88 72% 139.4 90% | 272 55 163 163 3 16 1 308 179 179 50 62 411 294 | 478 135 432 441 164 285 282 577 313 349 415 424 683 740 |
| HNGJ55 | 722240 | 416 | HMMER 2.1.1 blastx.2 | PFAM: MaoC like domain | PF01575 | 117.2 | 16 | 285 |
| HNGJ55 | 868063 | 869 | HMMER 2.1.1 | PFAM: MaoC like domain | PF01575 | 117.2 | 308 | 577 |
| HHGDG42 | 724795 | 417 | HMMER 2.1.1 blastx.2 | PFAM: Acetyltransferase (GNAT) family diamine N- acetyltransferase (EC 2.3.1.57) - spiny mouse (Mus saxicola) PFAM: ThiF family | PF00583 pir S43430 S43430 PF00899 | 24.9 40% 88 | 179 179 50 | 313 349 415 |
| HMTMF31 | 731302 | 418 | HMMER 2.1.1 blastx.2 | CG1749 PROTEIN. | sp Q9VYY3 Q9VYY 3 | 72% | 62 | 424 |
| HSDIF59 | 739212 | 419 | HMMER 2.1.1 blastx.2 | PFAM: Flavin reductase like domain 4- HYDROXYPHENYLAC | PF01613 sp P75893 P75893 | 139.4 90% | 411 294 | 683 740 |

| | | | | | | | | |
|---------|--------|-----|---------------------------|--|------------------------------|--|--|---|
| HNDAG60 | 751953 | 420 | HMME 2.1.1 blastx.2 | ETATE 3- MONOOXYGENASE (EC 1.14.13.3). PFAM: Kelch motif | PF01344 | 53.8 | 177 | 320 |
| | | | | NS1-BINDING PROTEIN. | sp Q9Y480 Q9Y480 | 67% 75% 100% 36% 32% 34% 28% 30% 33% | 174 296 3 174 174 174 323 174 320 418 | 425 445 80 323 320 320 436 320 418 |
| HSLDS79 | 733247 | 421 | HMME 2.1.1 blastx.2 | PFAM: Trehalase alpha, alpha-trehalase (EC 3.2.1.28) precursor, periplasmic - Escherichia coli | PF01204 pir S04782 S04782 | 1028.4 100% | 117 102 | 1622 1622 |
| HSLDS79 | 879215 | 870 | HMME 2.1.1 | PFAM: Trehalase | PF01204 | 102.4 | 132 | 392 |
| HFBCQ61 | 769102 | 422 | HMME 2.1.1 blastx.2 | PFAM: Kelch motif hypothetical protein W02G9.2 - Caenorhabditis elegans | PF01344 pir T33222 T33222 | 83.8 53% 41% 42% 37% 108.4 | 117 3 3 12 9 245 245 245 245 343 | 245 245 245 245 245 245 245 245 343 |
| HRACD17 | 769103 | 423 | HMME 2.1.1 | PFAM: Kelch motif | PF01344 | 108.4 | 245 | 343 |

| | | | | | | | | |
|---------|--------|-----|----------------|--|--------------------------|------------|----------|------------|
| | | | blastx.2 | CDNA FLJ10836 FIS, CLONE NT2RP4001228, WEAKLY SIMILAR TO 1 | sp BAA91845 BAA9 1845 | 94% | 2 | 358 |
| HLDQV23 | 788957 | 424 | HMMER 2.1.1 | PFAM: Glycosyl transferases | PF00535 | 59.7 | 71 | 364 |
| | | | blastx.2 | hypothetical protein F13G3.6 - Caenorhabditis elegans | pir T20856 T20856 | 42% | 68 | 376 |
| HPHAF45 | 812327 | 425 | HMMER 2.1.1 | PFAM: Kelch motif | PF01344 | 88.4 | 22 | 162 |
| | | | blastx.2 | CDNA FLJ10262 FIS, CLONE HEMBB1000985, WEAKLY SIMILAR TO 1 | sp BAA91514 BAA9 1514 | 100% | 118 | 384 |
| HSUME31 | 812373 | 426 | HMMER 2.1.1 | PFAM: Exonuclease | PF00929 | 118.4 | 4 | 441 |
| | | | blastx.2 | ISG20 PROTEIN. | sp O00441 O00441 | 57% | 1 | 441 |
| HUSHB56 | 815819 | 427 | HMMER 2.1.1 | PFAM: Calpain family cysteine protease | PF00648 | 70.1 | 101 | 346 |
| | | | blastx.2 | CALPAIN-LIKE PROTEASE. | sp Q9WVF0 Q9WVF 0 | 87% | 65 | 352 |
| HTGDN81 | 824708 | 428 | HMMER 2.1.1 | PFAM: RNB-like proteins | PF00773 | 395.6 | 417 | 1028 |
| | | | blastx.2 | virulence-associated protein vacB homolog - Escherichia coli | pir S56404 S56404 | 97% 94% | 417 1 | 998 435 |

| | | | | | | | | |
|---------|--------|-----|----------------------------|--|-------------------------------------|----------------------------|------------------------|---------------------------|
| HSKHY26 | 836598 | 429 | HMMER 2.1.1 blastx.2 | PFAM: Glycosyl transferases UDP- GALNAC:POLYPEPTID E.N- ACETYL GALACTOSA MINYLTRANSFERASE. | PF00535 sp Q9UIV5 Q9UIV5 | 66.5 | 35 | 427 |
| HKACD80 | 837698 | 430 | HMMER 2.1.1 blastx.2 | PFAM: Glycosyl hydrolase family 47 CDNA FLJ10783 FIS, CLONE NT2RP4000417, WEAKLY SIMILAR TO 1 | PF01532 sp BAA91806 BAA9 1806 | 125.1 | 198 | 521 |
| HHFDK48 | 837782 | 431 | HMMER 2.1.1 blastx.2 | PFAM: Sulfatase N-acetylgalactosamine-4- sulfatase (EC 3.1.6.12) precursor - cat | PF00884 pir A44475 A44475 | 143.6 | 13 | 351 |
| HE9SS77 | 838043 | 432 | HMMER 2.1.1 blastx.2 | PFAM: Sulfatase CG6725 PROTEIN. | PF00884 sp Q9VEX0 Q9VEX0 | 112.1 | 213 | 671 |
| HAPOK49 | 848205 | 433 | HMMER 2.1.1 blastx.2 | PFAM: UBA domain BS4 PROTEIN (NY- REN-18 ANTIGEN). | PF00627 sp Q9Y5A7 BS4_HU MAN | 61% 78.1 | 3 687 | 671 806 |
| HPMGN48 | 848318 | 434 | HMMER 2.1.1 blastx.2 | PFAM: Initiation factor 2 subunit family CG11334 PROTEIN. | PF01008 sp Q9V9X4 Q9V9X4 | 77% 71% 89% 264.5 | 195 833 47 75 | 872 1063 187 572 |
| | | | | | | 60% | 78 | 605 |

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|---------|--------|-----|----------------------------|---|--|----------------------------|--------------------------|----------------------------|
| HUVHP54 | 849278 | 435 | HMMER 2.1.1 blastx.2 | PFAM: Dienelactone hydrolase family Hypothetical 34.2 kDa protein. | PF01738 | 80.3 | 354 | 1001 |
| HSLDK59 | 853385 | 436 | HMMER 2.1.1 blastx.2 | PFAM: N- acetylmuramoyl-L-alanine amidase hypothetical protein b0867 precursor - Escherichia coli | sp AAG12612 AAG1 2612 PF01510 pir C64825 C64825 | 31% 80.6 100% 78% | 330 500 500 183 | 1001 736 1009 557 |
| HMWDI41 | 854051 | 437 | HMMER 2.1.1 blastx.2 | PFAM: Kelch motif CDNA FLJ20059 FIS, CLONE COL01349. | PF01344 sp BAA90921 BAA9 0921 | 91.2 92% | 488 2 | 595 592 |
| HFVHU73 | 856165 | 438 | HMMER 2.1.1 blastx.2 | PFAM: RNB-like proteins ribonuclease II RNB family protein - fission yeast (Schizosaccharomyces pombe) | PF00773 pir T38518 T38518 | 62.5 45% 38% | 6 9 253 | 281 281 360 |
| HMUBJ80 | 858497 | 439 | HMMER 2.1.1 blastx.2 | PFAM: Histone deacetylase family CDNA FLJ10328 FIS, CLONE NT2RM2000588, WEAKLY SIMILAR TO 1 | PF00850 sp BAA91545 BAA9 1545 | 44.9 93% 88% | 233 209 477 | 430 490 602 |
| HE9ML74 | 859297 | 440 | HMMER 2.1.1 blastx.2 | PFAM: HECT-domain (ubiquitin-transferase). CG5604 PROTEIN. | PF00632 sp Q9VL06 Q9VL06 | 74.3 82% | 705 940 | 914 1269 |

| | | | | | | | | |
|---------|--------|-----|----------------------------|--|-------------------------------------|---|--|--|
| HLQAJ01 | 864092 | 441 | HMMER 2.1.1 blastx.2 | PFAM: Histone deacetylase family Class I histone deacetylase. | PF00850 sp AAF73076 AAF73 076 | 40% 43% 24.3 | 456 3 13 | 932 350 90 |
| HSLDP32 | 866241 | 442 | HMMER 2.1.1 blastx.2 | PFAM: Fumarylacetoacetate (FAA) hydrolase family conserved hypothetical protein PA0318 [imported] - Pseudomonas aeruginosa (strain PAO1) | PF01557 pir G83604 G83604 | 100% 39.8 | 7 78 | 240 197 |
| HPMEG40 | 866272 | 443 | HMMER 2.1.1 blastx.2 | PFAM: Asparagine synthase asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - Escherichia coli | PF00733 pir A36616 AJECN | 244.9 72% 98% 87% | 270 270 31 589 | 590 656 267 636 |
| HRADE27 | 867195 | 444 | HMMER 2.1.1 blastx.2 | PFAM: Glycosyl transferases group 1 L165.1 (Fragment). | PF00534 sp AAF77213 AAF77 213 | 25 40% 44% | 125 50 385 | 403 409 531 |
| HTXQR10 | 869137 | 445 | HMMER 2.1.1 blastx.2 | PFAM: Kelch motif KELCH MOTIF CONTAINING PROTEIN. | PF01344 sp Q9Y2M5 Q9Y2M 5 | 94.1 44% 32% 43% 34% 36% | 283 166 166 181 166 181 | 423 381 531 366 381 363 |